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(54) Title: TRANSGENIC ORGANISM (57) Abstract <p>A transgenic organism is described which has an increased starch yield. The preferred embodiment concerns a plant or plant cell containing a recombinant DNA construct containing, in operational relationship to a plant promoter sequence or sequences enabling the expression of the gene by the plant or plant cell thereby to enhance the rate of production and/or yield of starch by the plant or the plant cell, a DNA sequence encoding an exogenous ADP glucose pyrophosphorylase enzyme (AGP) or a sub-unit thereof which retains the enzymatic activity of the AGP enzyme, characterised in that the said DNA sequence is the gene sequence, including non-critical allelic variations thereof, encoding the barley <i>Hordeum vulgare</i> endosperm AGP or an active sub-unit thereof, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequences defining the barley endosperm AGP or either of its sub-units.</p>		

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TRANSGENIC ORGANISM

The present invention relates to a transgenic organism.

5 In particular, the present invention relates to a transgenic starch producing organism having an increased ability to synthesize starch and one that is capable of producing starch in high yields. More particularly the present invention relates to a transgenic organism comprising a nucleotide sequence coding for exogenous ADP glucose pyrophosphorylase (AGP).

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In a preferred embodiment the present invention relates to a transgenic plant or plant cell capable of expressing exogenous AGP in the starch producing centres in the plant, namely the chloroplasts and the amyloplasts. The invention also relates to a recombinant DNA construct for use in the transformation of a plants or plant cell
15 showing enhanced starch production, and plants and plant cells transformed with the recombinant DNA construct.

ADP glucose pyrophosphorylase (E.C.2.7.7.27) (AGP) is one of the primary enzymes involved in the biosynthesis of starch and glycogen in organisms such as plants,
20 algae, fungi and bacteria, particularly plants.

AGP catalyses the reaction:



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the product ADP-glucose being the major donor of glucose in the biosynthesis of starch in plants. Moreover, that reaction has been shown to be the rate limiting factor in the synthesis of starch in organisms such as plants, the rate of that reaction in turn being critically dependent upon the AGP concentration. Because of that, AGP
30 has been the subject of intensive investigation and for a general review of recent studies on plant AGP, reference should be made to Kleczkowski et al: Z. Naturforsch. 46c, 605-612 (1991).

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As reported by Kleczkowski et al (*ibid*) and elsewhere, AGP is widely distributed throughout the plant kingdom and is found in some starch producing bacteria, such as E. coli. Plant AGP exists as a tetramer (210 to 240 kDa) composed of two small sub-units (50 to 55 kDa) and two large sub-units (51 to 60 kDa) in contrast to
5 bacterial AGP which appears to consist of four units of equal size. AGP has also been shown to be produced in cyanobacteria and in algae, where its tetrameric structure is similar to that in plants, i.e. two large and two small sub-units, rather than the homotetrameric structure found in ordinary bacteria.

10 Because of the commercial importance of starch, primarily as a foodstuff but also as an important industrial chemical, AGP itself and recombinant DNA constructs containing DNA sequences encoding AGP for the transfection of plants and plant cells as a means of increasing plant AGP concentration and hence increased biosynthesis of starch in plants and increased starch yields, have formed the subject matter of
15 several recently published patent applications.

For example, in EP-A-0368506 a method of extracting AGP from wheat leaf and wheat endosperm is disclosed. Also disclosed are the cDNA sequences encoding wheat leaf and wheat endosperm AGP, and various plasmids containing those
20 sequences for subsequent insertion into plants to provide plants having an increased ability to synthesise starch, although that latter step is not described in detail, nor are any examples given of transgenic plants containing those constructs.

WO 91/19806 discloses transformed plant cells and plants having elevated levels of
25 starch and starch biosynthesis achieved by incorporating into the plant genome a DNA construct comprising in sequence a plant promoter, a DNA sequence encoding a fusion polypeptide consisting of a plastid transit peptide and a bacterial (E. coli) AGP, and a 3'-non-translated region which functions in the plant cell to cause transcriptional termination and the addition of a polyadenylated tail to the 3'- end of
30 the corresponding DNA sequence. The DNA sequence encoding E. coli AGP is given, as well as the deduced amino acid sequence. Transgenic potato and tomato plants transformed with the E. coli AGP gene are shown to produce increased starch

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yields. It is suggested that other bacterial sources besides E. coli, and also algae, may be used as a source for the AGP gene to be used in the transformation of the plants and plant cells to provide increased starch yields. However, there is no mention of the isolation of nucleotide sequences coding for AGP enzymes from those
5 other sources or their expression in such transgenic systems.

A similar disclosure is contained in WO 92/11382 which likewise discloses the transformation of plants, especially potato plants, with bacterial (E. coli) DNA encoding bacterial AGP, with the objective of increasing starch biosynthesis and
10 starch yield in such plants.

A slightly different objective is set out in EP-A-0455316. There the objective is to increase sugar and protein concentrations in plant-based foodstuffs at the expense of starch formation. That is achieved by incorporating into the plant genome a DNA
15 sequence encoding AGP, but in an inverted orientation in the transformation vector. Transcription of the reversed sequence results in an anti-sense mRNA which inhibits the production of AGP in the plant cell leading to reduced AGP activity and reduced starch production.

20 All plant AGPs investigated so far have been reported to be strongly activated by 3-phosphoglycerate (PGA) and inhibited by inorganic phosphate (P_i). Also, the PGA/ P_i ratio in the chloroplasts and amyloplasts where biosynthetic starch production is concentrated is believed to play a key regulatory role in starch synthesis. It is known, for example, that chloroplast PGA/ P_i ratios are at the highest activity during
25 the daylight hours, i.e. during photosynthesis, which period coincides with the peak period of starch production in the chloroplasts. The regulation of the AGP formation in non-photosynthetic tissues is less well understood, but the activatory and inhibitory roles of PGA and P_i , respectively, i.e. the PGA/ P_i ratio, is believed still to play an important part.

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The present invention addresses the problem of how to increase AGPase levels and/or starch levels in starch producing organisms.

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According to a first aspect of the present invention there is provided a transgenic starch producing organism comprising a nucleotide sequence coding for an exogenous ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof which retains the enzymatic activity of the AGP enzyme, wherein the nucleotide sequence is capable of being expressed in the organism; characterised in that the activity of the enzyme or sub-unit thereof is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate; and further characterised in that the activity of the enzyme or sub-unit thereof is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

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According to a second aspect of the present invention there is provided a transgenic starch producing organism comprising exogenous ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof which retains the enzymatic activity of the AGP enzyme, wherein the activity of the enzyme or sub-unit thereof is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate and wherein the activity of the enzyme or sub-unit thereof is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

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According to a third aspect of the present invention there is provided a potato tuber containing an enhanced starch content.

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According to a fourth aspect of the present invention there is provided a method of increasing the rate and/or yield of starch production in an organism, especially a plant or a plant cell, which method comprises introducing into an organism a nucleotide sequence according to the present invention to form a transgenic organism according to the present invention and expressing the nucleotide sequence.

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According to a fifth aspect of the present invention there is provided a method of increasing the rate and/or yield of starch production in an organism, especially a plant or a plant cell, which method comprises introducing into or forming in an organism a ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof according to the present invention.

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According to a sixth aspect of the present invention there is provided any one of the following: A cDNA sequence identified herein as SEQ ID No. 2, including non-critical allelic variations of that sequence; An amino acid sequence as shown in SEQ ID No. 4, including variants thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence; A cDNA sequence identified herein as SEQ ID No. 5 including non-critical allelic variations of that sequence; An amino acid sequence as shown in SEQ ID No. 6, including variants thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.

10

According to a seventh aspect of the present invention there is provided any one of the following plasmids: Plasmid pPPS1; Plasmid pPPL1; Plasmid pPPL1M; Plasmid pPPS4; Plasmid pPPL4; Plasmid pPPL5; Plasmid pBKL4; Plasmid pVictor IV GN.

15 According to an eighth aspect of the present invention there is provided a method of increasing the rate and/or yield of starch production in an organism, especially a plant or a plant cell, which method comprises introducing into an organism a recombinant DNA construct containing an exogenous DNA sequence encoding an exogenous ADP glucose pyrophosphorylase enzyme (AGP) or sub-unit thereof and one or more
20 promoter sequences enabling the expression of the AGP encoded by that sequence by the organism thereby to increase the AGP content of the organism and in consequence to increase the rate of starch production by the organism and/or the starch yield, characterised in that the said DNA sequence is the gene sequence encoding the barley (Hordeum vulgare) endosperm AGP or a sub-unit thereof, or a variant thereof having
25 non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequences defining the barley endosperm AGP or either of its sub-units, wherein the construct is expressed in the organism; characterised in that the activity of the enzyme or sub-unit thereof is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate; and further
30 characterised in that the activity of the enzyme or sub-unit thereof is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

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According to a ninth aspect of the present invention there is provided a vector for the transformation of an organism, especially a plant or a plant cell, to increase the AGP content of such an organism consequently to increase the rate of starch production by such an organism, such vector comprising a recombinant DNA construct containing

5 a DNA sequence encoding an exogenous ADP glucose pyrophosphorylase enzyme (AGP), such vector also incorporating the necessary promoter and other sequences enabling the expression of that exogenous AGP in an organism transformed by that vector, characterised in that the said DNA sequence is the gene sequence encoding the barley (Hordeum vulgare) endosperm AGP or a sub-unit thereof, or a variant

10 thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequences defining the barley endosperm AGP or either of its sub-units, wherein the construct is capable of being expressed in the organism; characterised in that the activity of the enzyme or sub-unit thereof is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of

15 inorganic phosphate; and further characterised in that the activity of the enzyme or sub-unit thereof is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

According to a tenth aspect of the present invention there is provided a method of

20 targeting an exogenous protein to the amyloplast of plants or plant cells which comprises introducing into the plant or plant cell a recombinant DNA construct containing a DNA sequence encoding a starch branching enzyme transit peptide and an exogenous DNA sequence encoding the exogenous protein; wherein the construct is capable of being expressed in the plant or plant cells; preferably wherein the DNA

25 sequence encoding the starch branching enzyme comprises the sequence identified as SEQ.ID.No.5 and/or the starch branching enzyme expressed in the plant or plant cell by said construct comprises the amino acid sequence identified as SEQ.ID. No. 6.

According to an eleventh aspect of the present invention there is provided an AGP

30 enzyme or sub-unit thereof whose *in vivo* activity is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of P_i, and whose activity is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

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According to a twelfth aspect of the present invention there is provided a foodstuff made from or comprising an organism according to the present invention; preferably wherein the foodstuff is a fried foodstuff; more preferably wherein the foodstuff is a potato.

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The term 'transgenic organism' in relation to the present invention means an organism comprising an expressable exogenous nucleotide sequence or an expressed product of such an expressable exogenous nucleotide sequence. Preferably the expressable exogenous nucleotide sequence is incorporated in the genome of the organism.

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The term 'organism' in relation to the present invention includes any starch producing organisms such as plants, algae, fungi and bacteria, as well as cells thereof. Preferably the term means a plant or cell thereof, more preferably a potato and especially a potato tuber.

15

The term 'nucleotide' in relation to the present invention includes genomic DNA, cDNA, synthetic DNA, and RNA. Preferably it means DNA, more preferably cDNA.

20 The terms 'allele' and 'variant' in relation to the present invention mean any
; substitution of, variation of, modification of, replacement of, deletion of or the
addition of one or more nucleic acid(s)/amino acids from or to the sequence providing
the resultant sequence expresses or exhibits the required enzymatic activity. They
also mean a substantial homologous sequence wherein there is homology with respect
25 to at least the essential nucleic acids/nucleic acid residues/amino acids for expression
of or exhibition of the required enzymatic activity. Preferably there is at least 80%
homology, more preferably at least 90% homology, and even more preferably there
is at least 95% homology with the listed sequences. Hybrid sequences are also
covered. These may be prepared from at least two different sources - e.g. the variant
30 may include a sequence from one source that gives the variant the independence *vis-a-*
vis the level of *in vivo* 3-phospho-glycerate and a sequence from another source that
gives the variant the independence *vis-a-vis* the level of *in vivo* P_i.

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The term 'sub-unit' in relation to the present invention means an active component of the enzyme that displays the required enzymatic activity. For example, in the case of AGP enzyme obtained from barley (Hordeum vulgare), which is a heterotetramer containing two large sub-units and two small sub-units, the term includes any one of those sub-units as well as combinations thereof as well as a shortened variant thereof.

The term 'retains enzymatic activity' in relation to the present invention means that the activity of the enzyme variant or sub-unit thereof is still substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate, but not necessarily to the same extent as the native enzyme.

The term 'substantially independent' in relation to the present invention means that the enzyme has a decreased sensitivity to levels of PGA and/or of inorganic phosphate, preferably at least to PGA. By way of example, in the absence of PGA the levels of AGPase activity of the native enzyme or sub-unit thereof are in the order of at least 0.002 units per mg protein, preferably at least 0.01 units per mg protein - when measured in *Bintje* potato tuber extract. Typically, in the case of the preferred barley AGP enzyme we have found that the AGPase levels of the large sub-unit are greater than the levels of the small sub-unit and are typically in the order of greater than 0.02 units per mg protein and can be in the order of 0.05 units per mg protein - when measured in *Bintje* potato tuber extract. This is in contrast to the known enzymes which have no, or at most negligible, AGPase activity in the absence of PGA.

Preferably the enzymatic activity of the AGP enzyme is at least substantially independent of any level of *in vivo* 3-phospho-glycerate.

More preferably the enzymatic activity of the AGP enzyme is not stimulated by fructose-1,6-bisP and it is not inhibited by AMP.

Preferably the AGP enzyme is a heteromer, preferably a heterotetramer, more preferably a heteromer containing two large sub-units and two small sub-units.

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Preferably the AGP enzyme is isolatable from Hordeum, preferably wherein the enzyme is barley (Hordeum vulgare) endosperm AGP or a sub-unit thereof, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequences defining the barley endosperm AGP or either
5 of its sub-units.

Preferably the nucleotide sequence is a DNA sequence.

Preferably the DNA sequence encodes the large sub-unit of the barley endosperm
10 AGP or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequence defining the large sub-unit of the barley endosperm AGP.

Preferably the DNA sequence is the sequence identified herein as SEQ ID No 1,
15 including non-critical allelic variations of that sequence.

Preferably the DNA sequence encodes the small sub-unit of the barley endosperm AGP, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequence defining the small sub-unit of the
20 barley endosperm AGP.

Preferably the DNA sequence is the sequence identified herein as SEQ ID No 2, including non-critical allelic variations of that sequence.

25 Preferably both of the DNA sequences are expressed in the same organism. The DNA sequences need not be derived from the same initial source, such as barley. It is preferred however that they are from the same source, for example barley.

Preferably, when both of the DNA sequences are expressed in the same organism,
30 each DNA sequence additionally codes for a different marker - e.g. the large or small sub-unit of barley AGP enzyme may be in a construct that contains a kanamycin resistance gene such as a construct based on plasmid pBKL4 or pVictor IV GN and

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another small or large sub-unit of barley AGP enzyme may be in a construct that contains a mannose isomerase gene such as a construct based on plasmid pVictor IV SGIN Man.

- 5 Preferably the expressed AGP enzyme or sub-unit thereof comprises the amino acid sequence set out in SEQ ID No. 3, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.

- 10 Preferably the expressed AGP enzyme or sub-unit thereof comprises the amino acid sequence set out in SEQ ID No. 4, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.

- 15 Preferably the expressed AGP comprises both a large sub-unit having the amino acid sequence set out in SEQ ID No. 3 or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence, and a small sub-unit having the amino acid sequence set out in SEQ ID No. 4 or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.

- 20 Preferably the nucleotide sequence additionally codes for a transit peptide which can transport, or assist in the transportation of, the enzyme or sub-unit thereof from the cytoplasm to the relevant or appropriate plastid(s), such as a chloroplast and/or an amyloplast. Preferably the transit peptide is Rubisco Activase transit peptide or Starch Branching enzyme transit peptide.

- 25 Preferably the transit peptide is coded for by a DNA sequence comprising the sequence identified as SEQ. I.D. No. 5, including non-critical allelic variations of that sequence.

- 30 Preferably the transit peptide has an amino acid sequence comprising the sequence identified as Seq.I.D.No. 6, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.

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Preferably the nucleotide sequence is operatively connected to a promoter which expresses the sequence wherein the promoter is cell, tissue or organ specific.

5 Preferably the promoter has the sequence identified as SEQ.I.D.No.7, or a variant thereof having non-critical nucleotide substitution(s) or deletion(s) at one or more locations in that sequence.

10 Preferably the AGP enzyme or sub-unit thereof comprises the amino acid sequence set out in SEQ ID No. 3, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence and/or the amino acid sequence set out in SEQ ID No. 4, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.

15 Preferably the organism is a transgenic plant.

Preferably the transgenic plant is a potato plant.

20 Preferably the nucleotide sequence according to the present invention is obtainable from any one of the following plasmids: Plasmid pVictor IV SGiN Man; Plasmid pPPS1; Plasmid pPPL1; Plasmid pPPL1M; Plasmid pPPS4; Plasmid pPPL4; Plasmid pPPL5; Plasmid pBKL4; Plasmid pVictor IV GN.

Preferably the enzyme is obtainable from a eukaryotic source.

25 The present invention has broad applicability to starch producing organisms, especially plants. The present invention works better in organisms such as plants compared to bacteria.

30 In particular the present invention works better in plants compared to E. Coli where AGP activity is stimulated by fructose-1,6-bisP and inhibited by AMP. This E. Coli pathway is different to the pathway for the biosynthesis of starch in plants and algae.

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With regard to one preferred aspect of the present invention, namely a foodstuff prepared from frying a potato according to the present invention, it is to be noted that the increased starch content of the potato will lead to less fat/oil uptake during frying. This results in obvious dietary advantages. Moreover, the increased levels of starch
5 also means that there are decreased free levels of reducing carbohydrates - which are used in starch synthesis - and so there is a decreased tendency for the resultant product to become discoloured on frying by example reaction of the reducing carbohydrates with the hot fat/oil.

10 In accordance with a preferred aspect of the present invention it was found that AGP from barley (Hordeum vulgare) endosperm is highly active even in the absence of the activator PGA and is relatively insensitive to PGA/P_i ratios which play an important regulatory function in the case of AGP from most other known plant sources. The PGA/P_i ratio is also believed to play an important regulatory function in non-plant
15 AGP, e.g. algal AGP.

The cDNA sequences encoding parts of the large and the small sub-units of the barley endosperm AGP and the deduced amino acid sequences have recently been established and published in Plant Molecular Biology, 19, 381-389 (1992). The complete DNA
20 sequence encoding the large sub-unit together with the cDNA for the large sub-unit are set out in Plant Physiol. 100, 1617-1618, (1992).

In accordance with the present invention the complete DNA sequence encoding the small sub-unit of the barley endosperm AGP and the deduced amino acid sequence
25 has now been established. Those complete cDNA sequences are reproduced herein as SEQ ID Nos 1 and 2 encoding, respectively, the large and small sub-units of the barley endosperm AGP, whilst the deduced amino acid sequences are set out herein as SEQ ID Nos 3 and 4, respectively.

30 Thus, in the preferred embodiment of the present invention, it was discovered that starch production in plants can be enhanced/increased by incorporating into the plant's genome and under the control of suitable promoter sequence or sequences

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promoting the expression of the gene in the plant cells, particularly in the chloroplasts and amyloplasts, DNA sequences encoding either the large (60 kDa) sub-unit of barley (Hordeum vulgare) endosperm AGP or the small (51 kDa) unit, or both.

- 5 Thus, in a highly preferred aspect of the present invention there is provided transgenic plants and plant cells having increased rates of starch production and/or starch content, as compared with the corresponding non-transformed plant or plant cell, such plants and plant cells having been transformed with a recombinant DNA construct containing, in operational relationship (particularly in downstream
10 relationship) to a plant promoter sequence or sequences enabling the expression of the gene in the plant or plant cell, the gene sequence encoding the barley (Hordeum vulgare) endosperm AGP or an active sub-unit thereof retaining the enzymatic activity of the heterotetrameric AGP, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in the amino acid sequences
15 defining the barley endosperm AGP or either of its sub-units.

Whilst, in accordance with the present invention, a wide variety of organisms (e.g. plants and plant cells) may be transformed (especially with the gene encoding barley endosperm AGP or either of its sub-units) to increase starch production and starch
20 yields in that particular organism, the preferred embodiment concerns the transformation of the major starch producing plant crops, namely potato, rice, wheat and maize, which four crops in terms of calorific value, probably account for three quarters of the world's food supply. Sugar beet may also be transformed.

- 25 In a more specific aspect of the present invention there are provided transgenic plants and plant cells having increased rates of starch production and/or providing increased starch yields compared with the non-transformed material, such plants and plant cells having been transformed with a recombinant DNA construct containing in downstream relationship to a plant promoter sequence or sequences enabling the
30 expression of the gene in the transformed plant or plant cells, either or both the sequences SEQ ID No 1 and SEQ ID No 2 as set out in the prescribed fashion in the sequence listings annexed hereto and which are taken to be part of the present

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specification, or an allelic variant of either sequence showing substantial homology with the listed sequence and containing non-critical nucleotide substitutions at one or more locations in the nucleotide chain.

- 5 Alternatively defined, there are provided, in accordance with the present invention, transgenic plants and plant cells showing enhanced levels of AGP production, particularly, in the chloroplasts and amyloplasts, such plants and plant cells having been transformed with a recombinant DNA construct enabling the expression within the plant or plant cells of barley endosperm AGP or either of its sub-units, those sub-
- 10 units having the derived amino acid sequences set out in SEQ ID Nos. 3 and 4, or a variant of such a sequence having non-critical amino acid substitution(s) or deletion(s) at one or more locations in the amino acid sequence defining the barley endosperm AGP or either of its sub-units.
- 15 Also provided in accordance with this invention are plant transformation vectors for the transformation of plants and plant cells to increase the AGP content of such plants and plant cells and thus to increase the rate of production of starch by the transformed plant or plant cell and/or the starch yield, such vectors containing one or more promoter sequences functional in plants linked in operational relationship with a DNA
- 20 sequence encoding barley endosperm AGP, or either of its sub-units. More especially plant transformation vectors are provided comprising one or more promoter sequences functional in plants linked in operational relationship with either or both the sequences SEQ ID No 1 or SEQ ID No 2, or an allelic variant of either sequence showing substantial (at least 80%) homology with the listed sequence but having non-critical
- 25 nucleotide substitution(s) at one or more locations in the nucleotide chain.

With regard to the promoter, numerous promoters which are functional in plants are known. The promoter should be capable of allowing sufficient expression to result in the desired increase in starch production. Preferably, the promoter should be chosen

30 so that the increased starch production is carried out in the plant tissues where the starch production is required. For instance the promoters of starch biosynthetic genes from plants may be useful.

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Known examples of such promoters include the promoter of the granule bound starch synthase gene from potato (Van der Leij et al. [1991] Mol. Gen. Genet. 228: 240-248), and the promoter of the starch branching enzyme gene Sbe 1 from rice (Kawasaki et al. [1993] Mol. Gen. Genet. 237: 1-16).

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For expression in potato, a tuber specific class I patatin promoter is preferred (Mignery et al. [1988] Gene. 62: 27-44). The DNA sequence encoding the tuber specific class I patatin promoter is set out in the appendix hereto as SEQ ID No. 7. This patatin promoter was obtained from Dr. William Belknap, USDA - ARS,
10 Alabany, California.

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The DNA sequence encoding barley endosperm AGP is preferably linked to other control sequences for the expression of the DNA in addition to a promoter sequence such as a transcription terminator sequence. Transcription terminators may be derived from a variety of different genes, including plant, viral and Agrobacterium
genes. A cauliflower mosaic virus 35S terminator is preferred.

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AGP activity can occur in different sites in plants. For example in potatoes AGP activity is mainly localised in the chloroplasts (i.e. plastids specialising in photosynthesis) or the amyloplasts (i.e. plastids specialising in starch storage). Many amyloplast-localised proteins are expressed as precursors and are targeted to the amyloplast by an appropriate transit peptide that is subsequently removed. Similarly, many chloroplast-localised proteins are expressed as precursors which can be targeted to the chloroplast by an appropriate target peptide.

25

Whilst not wishing to be bound by any theory, it is believed that both the large and small sub-units of the barley endosperm AGP are synthesised as precursor peptides. Additional sequences are found to be attached to the amino-termini of the mature proteins which are understood to represent transit peptides. The transit peptide is then
30 cleaved upon sequestration of the precursor protein into the plastid. It is understood that the enzyme is not subjected to any other post-translation modification process *in vivo*.

- 16 -

However, in another embodiment of the present invention, it is desirable for the AGP transit peptides to be supplemented with one or more additional transit peptides. The transit peptide can be conveniently fused directly at the amino terminal methionine of the AGP barley sub-unit. In further preferred embodiments the barley AGP transit peptide can be substituted by another amyloplast or chloroplast transit peptide. The barley endosperm AGP cDNA is inserted into a convenient cloning vector, e.g. a plasmid, at a suitable restriction site. The DNA sequence of interest can be encloned into further vectors, if necessary, for the incorporation of additional DNA sequences. Suitable plant transit peptides include known chloroplast (Gavel & Von Heine [1990] FEBS Lett. 261: 455-458) or amyloplast (Van der Leij et al. [1991] Mol. Genet. 228: 240-248; Klosgen et al. [1989] Mol. Gen. Genet. 217: 155-161; Brisson et al. The Plant Cell [1989] 1: 559-566) transit peptides.

In potatoes, preferably a rubisco activase transit peptide (Werneke et al. Proc. Natl. Sci. USA [1988] 85: 787-791) or a starch branching enzyme transit peptide is used. The 480 bp starch branching enzyme cDNA sequence from potato showing 120 nucleotides of the 5' untranslated region and 360 nucleotides of the coding region (see SEQ.I.D. No. 5), which contains a putative 75 amino acid transit peptide and 45 amino acids of the mature branching enzyme is set out in the appendix hereto as SEQ ID No. 6.

In addition to the transit peptide portion of a protein, it may be desirable to include sequences encoding a portion of the mature plastid-targeted protein to further facilitate intracellular transport.

Preferably the plasmids are also provided with selection markers to enable the transformed plant cells to be separated out from plant cells which have not been transformed. Suitable genes are known and include e.g. a neomycin phosphotransferase gene (e.g. neo npt II), a phosphinotricine/bialaphos acetyltransferase gene (e.g. bar) and a β -glucuronidase gene (e.g. uidA) or a phosphomannose isomerase gene (e.g. manA, pmi).

- 17 -

In a preferred embodiment, the transformation vectors may be prepared by initially obtaining cDNA encoding the small and large units of barley endosperm AGP by the method described in Plant Molecular Biology, 19, 381-389 (1992). For ligation into a convenient cloning vector, e.g. a plasmid, the barley endosperm AGP cDNA is provided with restriction sites at each end by PCR using the oligonucleotide primers obtained by conventional oligonucleotide synthesis procedures or a commercially available oligonucleotide synthesizer such as, for example, Applied Biosystems 381 A DNA synthesizer. These restriction sites should be homologous with sequences in the cloning vector. The desired DNA sequence can be recloned into further vectors for preparation of the ultimate transformation vectors for preparing the transgenic starch producing organism, especially a transgenic plant.

In the preferred embodiment of the present invention, the plant or plant cells may be transformed by any suitable technique for transforming cells - such as use of T-DNA, electroporation, injection, DNA bombardment or fusion. After transformation, a whole plant can be cultivated from a transformed plant cell in the usual manner.

Preferably, transformation of the plant cell is achieved with T-DNA using *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*. If agrobacteria are used for transformation, the barley endosperm cDNA needs to be incorporated initially into either an intermediate vector or a binary vector. The intermediate vectors can be integrated into *Agrobacterium tumefaciens* by means of a helper plasmid. Preferably binary vectors are used, which can be transformed directly into agrobacteria. Binary vectors comprise a selection marker gene and a linker or polylinker which are framed by the right and left T-DNA border regions. The agrobacteria used as host cell should comprise a plasmid carrying a vir region, which is necessary for the transfer of the T-DNA into the plant cell. Transformation using *Agrobacterium* is achieved by cultivating the *Agrobacterium* with the plant cell.

Depending on the plant species to be transformed, a variety of different plant transformation vectors can be used. These include pBIN 121, pAL4404, pEHA101, pBKL4, pVictor IV SGiNMan and pVictor IV GN.

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For the transformation of potato species *Agrobacteria* the preferred plant transformation vectors are the plasmids pBK1.4, pVictor IV SGINMan and pVictor IV GN. These plasmids are described later in greater detail.

- 5 Preferred plasmids used in the construction of the plasmid used for transformations include pPATA1 and pBluescript II KS. Plasmid pBluescript II KS is a widely used cloning vector available from Stratagene.

Plants can be confirmed as transformed by performing conventional blotting assays
10 and PCR.

The starch content of the plants can be analysed based upon the specific gravity determined using the weight in water and the weight in air as described by W.A. Gould In: Chipping Potato Handbook, ed. Gould, W.A. The Snack Food Association,
15 Vermont, 1989, pp 18-22, in an article entitled "Specific gravity, its measurement and use.

The limitation of the exogenous ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof which retains the enzymatic activity of the AGP enzyme being not
20 stimulated by fructose-1,6-bisP and/or not inhibited by AMP, which further distinguishes the present invention from the AGP enzymes of the prior art such as those of WO 91/19806 and WO 92/11382, can be expressed in the alternative as either the exogenous ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof which retains the enzymatic activity of the AGP enzyme not being only just
25 an *E. Coli* AGP enzyme, or the exogenous ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof which retains the enzymatic activity of the AGP enzyme being capable of catalysing the reaction



30

- 19 -

The following samples were deposited in accordance with the Budapest Treaty at the recognised depositary The National Collections of Industrial and Marine Bacteria Limited (NCIMB) at 23 St. Machar Drive, Aberdeen, Scotland, United Kingdom, AB2 1RY on 29 March 1994:

5

E. Coli containing plasmid pPPS1 (NCIMB 40618);

E. Coli containing plasmid pPPL1 (NCIMB 40619);

10 *E. Coli* containing plasmid pPPS4 (NCIMB 40620);

E. Coli containing plasmid pPPL4 (NCIMB 40621); and

E. Coli containing plasmid pPPL5 (NCIMB 40622).

15

The following samples were deposited in accordance with the Budapest Treaty at the recognised depositary The National Collections of Industrial and Marine Bacteria Limited (NCIMB) at 23 St. Machar Drive, Aberdeen, Scotland, United Kingdom, AB2 1RY on 31 March 1994:

20

E. Coli containing plasmid pBKL4 (NCIMB 40623);

E. Coli containing plasmid pVictor IV GN (NCIMB 40624); and

25 *E. Coli* containing plasmid pVictor IV SGiN Man (NCIMB 40625).

A detailed construction of plant transformation vectors according to the present invention and the transformation of plants and plant cells using those vectors to produce transgenic plants according to this invention having increased rates of starch
30 biosynthesis and/or starch yield will now be described in more detail.

- 20 -

In this regard, the present invention will now be described only by way of example.

In the following Examples reference is made to the accompanying figures in which:

- 5 Figure 1 shows the restriction map for plasmid pPATA1;
 Figure 2 shows the restriction map for plant transformation vector pBK14;
 Figure 3 shows the restriction map for plasmid pPPS1;
 Figure 4 shows the restriction map for plasmid pPPL1;
 Figure 5 shows the restriction map for plasmid pATP1;
- 10 Figure 6 shows the restriction map for plant transformation vector pVictor IV GN;
 Figure 7 shows the restriction map for plant transformation vector pVictor IV SGIN
 Man;
 Figure 8 shows the N terminal amino acid sequence of the rubisco activase - AGP
 small subunit fusion enzyme, the N terminal amino acid sequence of the rubisco
15 activase - AGP large subunit fusion enzyme and the N terminal amino acid sequence
 of the starch branching enzyme - AGP large subunit fusion enzyme;
 Figure 9 shows the restriction map for plasmid pPPS4;
 Figure 10 shows the restriction map for plasmid pBETP5;
 Figure 11 shows the restriction map for plasmid pPPL4;
- 20 Figure 12 shows the restriction map for plasmid pPPL5;
 Figure 13 shows the restriction map for plasmid pPPL1M;
 Figure 14 shows the cDNA and amino acid sequences for the large sub-unit of barley
 AGP;
 Figure 15 shows the cDNA and amino acid sequences for the small sub-unit of barley
25 AGP;
 Figure 16 shows the cDNA (first 480 nucleotides from 5' end) and amino acid (first
 120 amino acids from amino terminus) sequences for the starch branching enzyme;
 and
 Figure 17 shows the genomic DNA sequence for the preferred potato promoter.

In the following Examples the following amino acid codes are used:

5

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Symbol	3-letter	Meaning
A	Ala	Alanine
B	Asp, Asn	Aspartic Asparagine
C	Cys	Cysteine
D	Asp	Aspartic
E	Glu	Glutamic
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
V	Val	Valine
W	Trp	Tryptophan
X	Xxx	Unknown
T	Tyr	Tyrosine
Z	Glu, Gln	Glutamic Glutamine
+	End	Terminator

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A. Construction of plant transformation vectors containing the ADP-glucose pyrophosphorylase genes expressed from a patatin class I promoter

EXAMPLE 1

5

Plasmid pPPS1

Plasmid pPPS1 is a pBKL4 derivative containing the construction:

- 10 Patatin promoter - small sub-unit AGP cDNA - 35S terminator

The AGP cassette was inserted in the KpnI site of pBKL4. The additional elements introduced in the pBKL4 T-DNA by this insertion are described below.

- 15 **Patatin promoter:** The patatin promoter is a tuber specific promoter from potato (Mignery et al. 1988, Gene 62:27-44) - see SEQ. ID. No. 7.

- Small subunit ADP-glucose pyrophosphorylase (bepsF2):** This is a 1.8 kb cDNA fragment encoding the small subunit ADP-glucose pyrophosphorylase from barley
20 endosperm - see SEQ ID. No. 2.

35S terminator: The CaMV 35S terminator (Odell et al. 1985, Nature 313:810-812) is fused to the bepsF2 fragment.

- 25 In more detail, a 1.8 kb BamHI cDNA fragment encoding the barley endosperm ADP glucose pyrophosphorylase small subunit (beps) was cloned in the BamHI site of plasmid pPATA 1 (Figure 1). Plasmid pPATA 1 is a derivative of plasmid pUC19 and has tuber specific patatin class I promoter ID SEQ No. 7, a polylinker cloning region, and a 35S terminator. From the resulting plasmid the 3.1 kb KpnI fragment
30 containing the patatin promoter, the beps cDNA and the 35S terminator was isolated and inserted in the KpnI site of the plant transformation vector pBKL4 (Figure 2) to yield plasmid pPPS1 (Figure 3).

- 23 -

Plasmid pBKL4 is a derivative of plasmid pBIN19 for Agrobacterium tumefaciens mediated transformation of plants and harbours a T-DNA region with a β -glucuronidase gene (GUS) transcribed from a 35S promoter and terminated at the nopaline synthase gene terminator, a polylinker cloning region, and a
5 neophosphotransferase gene transcribed from a 35S promoter and terminated at the octopine synthase gene terminator.

EXAMPLE 2

10 **Plasmid pPPL1**

Plasmid pPPL1 is a pBKL4 derivative containing the construction:

Patatin promoter - Large subunit ADP-glucose pyrophosphorylase cDNA - 35S
15 terminator.

The ADP-glucose pyrophosphorylase cassette was inserted in the EcoRI site of pBKL4.

20 The additional elements introduced in the pBKL4 T-DNA by this insertion are described below.

Patatin promoter: The patatin promoter is a tuber specific promoter from potato (Mignery et al. 1988, Gene 62:27-44) - see SEQ. ID. No. 7.

25

Large subunit ADP-glucose pyrophosphorylase (bep110): This is a 1.9 kb cDNA fragment encoding the large subunit ADP-glucose pyrophosphorylase from barley endosperm (Villand et al. 1992, Plant Physiol 100:1617-1618) - see SEQ ID. No. 1.

30 **35S terminator:** The CaMV 35S terminator (Odell et al. 1985, Nature 313:810-812) is fused to the bep1 10 fragment.

- 24 -

In more detail, a 1.9 kb EcoRI-HindIII cDNA fragment encoding the barley endosperm ADP glucose pyrophosphorylase large subunit (bepl) was isolated, the restriction ends were filled in with klenow DNA polymerase, and the blunt ended DNA fragment was cloned in the SmaI site of plasmid pPATA1. From the resulting
5 plasmid the 3.2 kb EcoRI fragment containing the patatin promoter, the bepl cDNA, and the 35S terminator was isolated and inserted in the EcoRI site of the plant transformation vector pBKL4 to yield plasmid pPPL1 (Figure 4).

EXAMPLE 3

10

Plasmid pPPL1M

Plasmid pPPL1M (see Figure 13) is similar to pPPL1 except that the ADP-glucose pyrophosphorylase cassette:

15

Patatin promoter - Large subunit ADP-glucose pyrophosphorylase - 35S terminator.

was inserted in the EcoRI site of pVictorIV SGN Man.

20 EXAMPLE 4

Plasmid pVictor IV SGN

pVictorIV SGN (Figure 6) is a vector for *Agrobacterium* mediated plant
25 transformation, and contains the Ti right and left border sequences from the nopaline type pTiT37 plasmid (Yadav et al. 1982, Proc Natl Acad Sci 79:6322-6326) flanking the genes encoding kanamycin resistance (NPTII) and β -glucoronidase (GUS).

For replication and maintenance in *E. coli* the plasmid contains the origin of
30 replication from the *E. coli* plasmid pUC19 (pUC19ori) Yanish-Perron et al. 1985 Gene 33:103-119), and for replication and maintenance in *Agrobacterium tumefaciens* the plasmid further contains the origin of replication from the *Pseudomonas* plasmid

- 25 -

pVS1 (pVS1ori) (Itoh et al. 1984, Plasmid 11:206-220, Itoh and Haas 1985, Gene 36:27-36). For selection in *E. coli* and *Agrobacterium tumefaciens* the plasmid contains the spectinomycin/streptomycin resistance gene (spec.strep) from the transposon Tn7 encoding the enzyme 3'(9)-O- nucleotidyltransferase (Fling et al. 1985, Nucleic Acids Res 19:7095-7106). The spec/strep resistance gene is fused to the *tac* promoter for efficient expression in the bacterium.

The T-DNA segment between the right and left border harbours the following genes, which are the only genes transferred to the potato plant via the *Agrobacterium tumefaciens* mediated transformation.

β -glucuronidase (GUS): This segment next to the right border is the β -glucuronidase gene (GUS) from *E. coli* (Jefferson et al., 1986, Proc Natl Acad Sci 83:8447-8451) fused to the CaMV 35S promoter (35S) and 35S terminator (35St) (Odell et al. 1985, Nature 313:810-812).

Multiple cloning sites (MCS): A polylinker containing various restriction endonuclease recognition sites is inserted after the 35S terminator.

Kanamycin resistance (NPTII): The segment next to the MCS is the kanamycin (neomycin) phosphotransferase gene (NPTII) from the transposon Tn5 (Beck et al. 1982 Gene 19:327-336) fused to the CaMV 35S promoter (Odell et al. 1985, Nature 313:810-812) and the terminator of the octopine synthase gene (Caplan et al. 1983, Science 222:815-821).

EXAMPLE 5

Plasmid pVictor IV SGiN Man

pVictorIV SGiN Man (Figure 7) is similar to pVictorIV SGN (Bilag XI) except that the GUS gene is replaced by another GUS gene containing an intron (GUSintron) to prevent expression in bacteria.

- 26 -

Moreover, the kanamycin (neomycin) phosphotransferase gene (NPTII) has been replaced by the mannose-6-phosphate isomerases gene, *manA*, from *E. coli*.

- 5 **β -glucuronidase (GUSintron):** This segment next to the right border is the β -glucuronidase gene (GUS) from *E. coli* (Jefferson et al. 1986, Proc Natl Acad Sci 83:8447-8451) furnished with an intron to prevent expression in bacteria, and fused to the CaMV 35S promoter (35S) and 35S terminator (35St) (Odell et al. 1985, Nature 313:810-812).
- 10 **Mannose-6-phosphate isomerase:** This segment is the mannose-6-phosphate isomerases gene, *manA*, from *E. coli* (Miles and Guest 1984, Gene 32:41-48) fused to the enhanced 35S promoter (E35S) (Kay et al. 1987, Science 236:1299-1302) and 35S terminator (35St) (Odell et al. 1985, Nature 313:810-812). The phosphomannose isomerase gene is used as a selection marker to select transgenic shoots on a media
- 15 containing D-mannose as the carbon source.

B. Attachment of transit peptides to the ADP-Glucose pyrophosphorylase subunits

20 **EXAMPLE 6**

Plasmid pPPS4

pPPS4 (Figure 9) is a pVictorIV derivative in which a 3 kb KpnI fragment containing

25 the construct

Patatin promoter - spinach rubisco activase transit peptide - small subunit AGP from barley endosperm - 35S terminator

30 is inserted in the KpnI site.

- 27 -

In more detail, the coding region of the barley endosperm ADP glucose pyrophosphorylase small subunit (beps) cDNA was amplified by PCR using the primers:

5' CGG GAT CCA TGG ATG TAC CTT TGG CA 3'

and

5' CGG GAT CCT TAT TTA TTT ATA TGA CTG TTC CAC TAG 3'

which provide the PCR fragment with a BamHI and a NcoI in the 5' end and a
 10 BamHI site at the 3' end. The 1.4 kb BamHI fragment containing the entire coding region of the AGP small subunit plus two additional amino acids (G and S) at the amino-terminal end was cloned in the BamHI site of pBluescript II KS to yield plasmid pBBSF. The 1.4 kb BamHI fragment was isolated from pBBSF and cloned in the BamHI site of plasmid pATP1 (Figure 5). Plasmid pATP1 has a patatin
 15 promoter, a 58 amino acid rubisco activase transit peptide DNA and 35 amino acids of the mature enzyme, a BamHI site that facilitates in frame fusion of the small subunit AGP reading frame, and a 35S terminator. The 3 kb KpnI fragment including the patatin promoter, the activase transit peptide, the AGP coding region, and the 35S terminator was isolated from the resulting plasmid and cloned in the KpnI
 20 site of the plant transformation vector pVictorIV GN (Figure 6) to give plasmid pPPS4 (Figure 9).

Amino terminal amino acid sequence of the rubisco activase - AGP small subunit fusion enzyme.

25

1 MATAVSTVGA ATRAPLNLNG SSAGASVPTS GFLGSSLKKH 40

41 TNVRFPSRR TTSMTVKAAE NEEKNTDKWA HLAKDFSDDQ 80

30 81 LDIRRGKGMV DSLGSM DVPL ASKVPLSPS KHEQCNVYSH 120

- 28 -

The rubisco activase sequences starts at amino acid residue 1 and ends at leucine residue at 93, while the AGP small subunit sequences begins with the methionine at 96. The rubisco activase transit peptide is cleaved at the alanine residue at 58 leaving the alanine at 59 as the N-terminal amino acid.

5

The above sequence is listed later on as SEQ.I.D. No. 8.

EXAMPLE 7

10 **Plasmid pPPL4**

pPPL4 is a pVictorIV SGiN Man derivative in which a 3.2 kb EcoRI fragment containing the construct

15 **Patatin promoter - spinach rubisco activase transit peptide - large subunit AGP from barley endosperm - 35 S terminator**

is inserted in the EcoRI site.

20 **In more detail, the coding region of the barley endosperm ADP glucose pyrophosphorylase large subunit (bepl) cDNA was amplified by PCR using the primers**

5' GCG GAT CCA TAT CGA GTT CAG CGT 3'

25 and

5' CGG GAT CCG CAC AGG TTG TCG CAG AAC 3'

30 **which provide the PCR fragment with a BamHI and a NdeI in the 5' end and a BamHI site at the 3' end. The 1.6 kb BamHI fragment containing the entire coding region of the AGP large subunit plus two additional amino acids (I and H) at the amino-terminal end was cloned in the BamHI site of pBluescript II KS to yield plasmid pBBLF.**

- 29 -

The 1.6 kb BamHI fragment was isolated from pBBLF and cloned in the BamHI site of plasmid pATP2. Plasmid pATP2 has a patatin promoter, a 58 amino acid rubisco activase transit peptide DNA and 35 amino acids of the mature enzyme, a BamHI site that facilitates in frame fusion of the large subunit AGP reading frame, and a 35S terminator. The 3 kb EcoRI fragment including the patatin promoter, the activase transit peptide, the AGP coding region, and the 35S terminator was isolated from the resulting plasmid and cloned in the EcoRI site of the plant transformation vector pVictor IV SGiN Man (Figure 7) to form plasmid pPPL4 (Figure 11).

10 **Amino terminal amino acid sequence of the rubisco activase - AGP large subunit fusion enzyme.**

```

1      MATAVSTVGA ATRAPLNLNG SSAGASVPTS GFLGSSLKKH 40
41     TNVRFPSSSR TTSMTVKAAE NEEKNTDKWA HLAKDFSDDQ 80
15    81     LDIRRGKGMV DSLGIHMQFS SVLPLEGKAC VSPVRREGSA 120

```

The rubisco activase sequences starts at amino acid residue 1 and ends at the leucine residue at 93, while the AGP large subunit sequences begins with the methionine at 97. The rubisco activase transit peptide is cleaved at the alanine residue at 58 leaving the alanine at 59 as the N-terminal amino acid. The above sequence is listed later on as SEQ.I.D. No. 9.

EXAMPLE 8

25 **Plasmid pPPL5**

pPPL5 is a pVictorIV GIN MAN derivative in which a 3.4 kb EcoRI fragment containing the construct

Patatin promoter - potato starch branching enzyme amyloplast transit peptide - large subunit AGP from barley endosperm - 35S terminator

is inserted in the EcoRI site.

- 30 -

The coding region of the barley endosperm ADP glucose pyrophosphorylase large subunit was amplified by PCR using the primers:

5' CGG GAT CCG ATG CAG TTC AGC AGC GTG 3'

5 and

5' CGG GAT CCG CAC AGG TTG TCG CAG AAC 3'

which provide a 1.62 kb PCR fragment with BamHI ends. The BamHI fragment containing the entire coding region of the AGP large subunit plus one additional amino acid (P) at the amino terminal end was inserted in the BamHI site of pBETP5 (Figure 10). In this way the AGP large subunit was fused to the 75 amino acid potato starch branching enzyme transit peptide plus 26 amino acids of the mature branching enzyme. The fusion enzyme is expressed from a patatin promoter and terminated at a 35S terminator. The 3.4 Kb EcoRI fragment from the resulting plasmid (pPBL1) containing the patatin promoter, the starch branching enzyme transit peptide-AGP large subunit fusion enzyme, and the 35S terminator, was inserted in the EcoRI site of the plant transformation vector pVictorIV SGiN Man yielding plasmid pPPL5 (Figure 12).

Amino terminal amino acid sequence of the starch branching enzyme - AGP large subunit fusion enzyme.

1 MEINFKVL SK PIRGSFPSFS PKVSSGASRN KICFPSQHST 40
41 GLKFGSQERS WDISSTPKSR VRKDERMKHS SAISAVLTDD 80
25 81 NSTMAPLEED VKTENIGLLN LDPMQFSSVL PLEGKACVSP 120

The starch branching enzyme sequences starts at amino acid residue 1 and ends at 103, while the AGP large subunit sequence begins with the methionine at 104. The starch branching enzyme transit peptide is cleaved at the alanine residue (75) leaving the valine residue (76) as the amino terminal amino acid.

The above sequence is listed later on as SEQ.I.D. No. 10.

C. Production of transgenic potato plants containing the AGP-gene

EXAMPLE 9

5 Axenic stock cultures

Shoot cultures of *Solanum tuberosum* ' Bintje ' and ' Dianella ' are maintained on a substrate (LS) of a formula according to Linsmaier, E.U. and Skoog, F. (1965), *Physiol. Plant.* 18: 100-127, in addition containing 2 μ M silver thiosulphate at 25°C and 16 h light/8 h dark.

The cultures are subcultured after approximately 40 days. Leaves are cut off the shoots and cut into nodal segments (approximately 0.8 cm) each containing one node.

15 Inoculation of potato tissues

Shoots from approximately 40 days old shoot cultures (height approximately 5-6 cms) were cut into internodal segments (approximately 0.8 cm). The segments are placed into liquid LS-substrate containing the transformed *Agrobacterium tumefaciens* containing the binary vector of interest. The *Agrobacterium* are grown overnight in YMB-substrate (dipotassiumhydrogen phosphate, trihydrate (0.66 g/l); magnesium sulphate, heptahydrate (0.20 g/l); sodium chloride (0.10 g/l); mannitol (10.0 g/l); and yeast extract (0.40 g/l)) containing appropriate antibiotics (corresponding to the resistance gene of the *Agrobacterium* strain) to an optical density at 660 nm (OD-660) of approximately 0.8, centrifuged and resuspended in the LS-substrate to an OD-660 of 0.5.

The segments are left in the suspension of *Agrobacterium* for 30 minutes and then the excess of bacteria are removed by blotting the segments on sterile filter paper.

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Co-cultivation

The shoot segments are co-cultured with bacteria for 48 hours directly on LS-substrate containing agar (8.0 g/l), 2,4-dichlorophenoxyacetic acid (2.0 mg/l) and trans-zeatin (0.5 mg/l). The substrate and also the explants are covered with sterile filter papers, and the petri dishes are placed at 25°C and 16 h light/ 8 dark.

"Washing" procedure

After the 48 h on the co-cultivation substrate the segments are transferred to containers containing liquid LS-substrate containing 800 mg/l carbenicillin. The containers are gently shaken and by this procedure the major part of the Agrobacterium are washed off the segments and/or killed.

Selection

After the washing procedure the segments are transferred to plates containing the LS-substrate, agar (8 g/l), trans-zeatin (1-5 mg/l), gibberellic acid (0.1 mg/l), carbenicillin (800 mg/l), and kanamycin sulphate (50-100 mg/l) or phosphinotricin (1-5 mg/l) or mannose (5 g/l) depending on the vector construction used.

The segments are sub-cultured to fresh substrate each 3-4 weeks.

In 3 to 4 weeks, shoots develop from the segments and the formation of new shoots continues for 3-4 months.

Rooting of regenerated shoots

The regenerated shoots are transferred to rooting substrate composed of LS-substrate, agar (8 g/l) and carbenicillin (800 mg/l).

- 33 -

The transgenic genotype of the regenerated shoot are verified by testing the rooting ability on the above mentioned substrates containing kanamycin sulphate (200 mg/l), by performing NPTII assays (Radke, S. E. et al, Theor. Appl. Genet. (1988), 75: 685-694) or by performing a GUS assay on the co-introduced β -glucuronidase gene according to Hodal, L. et al. Pl. Sci. (1992), 87: 115-122 or by assaying the for the expression of the barley AGP mRNA or AGP enzyme activity as described elsewhere. Plants which are not positive in any of these assays are discarded or used as controls.

Transfer to soil

10

The newly rooted plants (height approx. 2-3 cms) are transplanted from rooting substrate to soil and placed in a growth chamber (21°C, 16 hour light 200-400uE/m²/sec).

15 When the plants are well established they are transferred to the greenhouse, where they are grown until tubers have developed and the upper part of the plants are senescing.

Harvesting

20

The potatoes were harvested after about 3 months.

AGP Assay

25 Tubers from the harvested potato plants were stored at 4°C. AGPase was extracted by homogenization of 10-20g of thinly sliced potato tubers in 20 ml of buffer containing 25 mM Hepes (pH 7.4) mM mercaptoethanol and 1 mM DTT. Homogenization was performed at 0-4°C using 30 ml Waring blender at full speed for 15 seconds. Aliquots of crude extract were then immediately centrifuged at maximal speed for 1 min using bench Eppendorf microcentrifuge and then assayed for AGPase activity. Assays were carried out immediately after centrifugation to make sure that the enzyme will not be inactivated during storage.

- 34 -

Assays were carried out in the pyrophosphorolysis direction monitoring glucose-1-P formation at 340 nm (21°C), using LKB spectrophotometer (Ultrospec II). Assay mixtures (1 ml) contained: 100 mM Mops (pH 7.4), 0.6 mM NAD, 7mM $MgCl_2$, 1 mM ADP-glucose, 1 mM inorganic pyrophosphate, 10 uM glucose-1,6-biphosphate, 2 units each of glucose-6-P dehydrogenase and phosphoglucomutase. In some instances, 2 mM 3-phosphoglyceric acid (PGA) was added to assays. Assays were run (-PGA) for ca. 5 min, and then PGA was added and assays were monitored for another 5-10 min. Rates were usually linear during the time-course of assays. One unit of AGPase activity corresponds to the amount of enzyme producing 1 umole of NADH under assay conditions.

Starch Analysis

The starch contents of potato tubers was determined according to a method which was designed and proposed by the Dutch-German working group "Standardization" and published in "Methods of assessment for potatoes and potato products". The method was developed for use with a sample size of 5000 g but we scaled the method down for use with potato tubers from a single plant, usually between 20 and 200 g.

All potatoes from a plant are washed and dried with a cloth before weighing (a grams) on an electronic balance. Later, the tubers are weighed again, but this time on a balance with two metal baskets of which one is immersed in a water basin. The potato tubers are placed in the bucket in water, and their weight (b grams) in water is determined.

25

The under-water weight of a sample is calculated at $5000 \cdot b/a$ grams. From tables showing the relation between under-water weight, dry matter and starch content, the two latter figures can be determined.

This procedure is described in more detail by W.A. Gould in Chipping Potato Handbook, ed. Gould, W.A. The Snack Food Association, Vermont, 1989, pp 18-22, in an article entitled "Specific gravity, its measurement and use.

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RESULTS

AGPase levels and starch levels were increased with the constructs of the present invention, particularly in the absence of PGA, especially with the constructs coding for the large sub-unit and in particular the constructs coding for a transit peptide.

In this regard, some results are shown in Table I (below) for transformed potatoes comprising constructs derived from plasmids pPPS4 and pPPL4.

TABLE I
STARCH CONTENT IN TRANSFORMED POTATOES (TRANS)
COMPARED TO CONTROL NATIVE POTATOES
GROWN UNDER THE SAME CONDITIONS

Sample	% Overall Starch Content	%Starch Content vis-a-vis Control
Control	16	100
Trans 1	19	119
Trans 2	23	144
Trans 3	26	163
Trans 4	19	119
Trans 5	26	163
Trans 6	24	150
Trans 7	21	131
Trans 8	17	106
Trans 9	21	131

The above results clearly show that the average starch level in the transgenic potatoes comprising constructs derived from plasmids pPPS4 and pPPL4 are increased to about 136 % of that found in native potatoes.

Furthermore, the average starch level for the upper two quartiles for the transgenic potatoes comprising constructs derived from plasmids pPPS4 and pPPL4 is about 155 % of that found in native potatoes.

- 5 Each of these findings is significant.
- 10 Other modifications of the present invention will be apparent to those skilled in the art without departing from the scope of the invention.

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SEQUENCE LISTING

(1) GENERAL INFORMATION

- 5 NAME OF APPLICANTS: DANISCO A/S
 BUSINESS ADDRESS: Langebrogade 1
 DK-1001 Copenhagen K
 Denmark
- 10 TITLE OF INVENTION: TRANSGENIC ORGANISM

(2a) INFORMATION FOR SEQUENCE I.D. 1

- SEQUENCE TYPE: NUCLEIC ACID
- 15 MOLECULE TYPE: DNA
- ORIGINAL SOURCE: BARLEY
- SEQUENCE LENGTH: 2037
- STRANDEDNESS: DOUBLE
- TOPOLOGY: LINEAR
- 20 SEQUENCE: Nucleotide sequence of a cDNA encoding the large subunit of ADP-glucose pyrophosphorylase from barley seed endosperm (bep110)

25 SEQ. ID. No. 1

```

1   ACGACCACCT CCGAACTCAA CGCCTCCACG GACCATCTCT
41  CTCCTCTCCC CTCCCCTCAC CACCACCACC ACCACCACCC
81  CTTCCTCCCTC CCTGCATTG ATTGTTTCAT ATTCATCCGT
30 121 CGCTTGCCCG GTCGCCACCC CGTCGATCCC TCACCCCGCC
161 GTCCCCGGCA GTTGCAAGTG GACTGCTAAT GTCATCGATG
201 CAGTTCAGCA GCGTGCTGCC CCTGGAGGGC AAGGCGTGCG
241 TTCCCCAGT CAGGAGAGAG GGATCGGCCT GCGAGCGCCT
281 CAAGATCGGG GACAGCAGCA GCATCAGGCA CGAGAGAGCG
35 321 TCCAGGAGGA TGTGCAACGG CGGCGCAGGG GCCCCGCCGC
361 CACCGGTGCG CAGTGCGTGC TCACCTCCGA CGCCAGCCCC
401 GCCGACACCC TTGTTCTCCG GACGTCCTTC CGGAGGAATT
   ACGCCGATCC GAACGAGGTC GCGGCCGTCG GTCGCGGCCG
   TCATACTCGG CGGCGGCACC GGGACTCAGC TCTTCCCGCT
40  CACAAGCACA AGGGCCACAC CTGCTGTTCC TATTGGAGGA
   TGTTACAGGC TCATCGATAT TCCCATGAGC AACTGCTTCA
601 ACAGTGGCAT CAACAAGATA TTCGTCATGA CCCAGTTCAA
   CTCGGCATCT CTCAATCGCC ACATTCACCG CACCTACCTC
   GGCGGGGGAA TCAATTTAC TGATGGATCT GTTGAGGTAT
45  TGGCCGCGAC ACAAATGCCT GGGGAGGCTG CTGGATGGTT
   CCGCGGAACA GCGGATGCCG TCAGAAAATT TATCTGGGTG
801 CTTGAGGACT ACTATAAGCA TAAATCCATA GAGCACATTT
   TGATCTTGTC GGGCGATCAG CTTTATCGCA TGGATTACAT

```

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GGAGCTTGTG CAGAAACATG TGGATGACAA TGCTGACATT
ACTTTATCAT GTGCCCCTGT TGGAGAGAGC CGGGCATCTG
AGTACGGGCT AGTGAAGTTC GACAGTTCAG GCCGTGTGAT
1001 CCAGTTTTCT GAGAAGCCAA AGGGCGACGA TCTGGAAGCG
5 ATGAAAGTGG ATACCAGTTT TCTCAATTTT GCCATAGACG
ACCCTGCTAA ATATCCATAC ATTGCTTCGA TGGGAGTTTA
TGTCTTCAAG AGAGATGTTC TGCTGAACCT TCTAAAGTCA
AGATACGCAG AACTACATGA CTTTGGGTCT GAAATCCTCC
1201 CGAGAGCTCT GCATGATCAC AATGTACAGG CATATGTCTT
10 CACTGACTAC TGGGAGGACA TTGGAACAAT CAGATCCTTC
TTCGATGCGA ACATGGCCCT CTGCGAACAG CCTCCAAAGT
TTGAATTTTA TGATCCAAAA ACCCCCTTCT TCACTTCGCC
TCGGTACTTA CCGCCAACAA AGTCAGACAA GTGCAGGATC
1401 AAAGAAGCGA TCATTTTCGA CGGCTGCTTC TTGCGTGAAT
15 GCAAAATCGA GCACTCCATC ATCGGCGTTC GTTCACGCCT
AAACTCCGGA AGCGAGCTCA AGAACGCGAT GATGATGGGC
GCGGACTCGT ACGAGACCGA GGACGAGATC TCGAGGCTGA
TGTCTGAGGG CAAGGTTCCC ATCGGCGTCG GGGAGAACAC
1601 AAAGATCAGC AACTGCATCA TCGACATGAA CGCGAGGATA
20 GGAAGGGACG TGGTCATCTC AAACAAGGAG GGGGTGCAAG
AAGCCGACAG GCCGGAGGAA GGGTACTACA TCAGGTCCGG
GATCGTGGTG ATCCAGAAGA ACGCGACCAT CAAGGACGGC
ACCGTCGTGT AGGGCGTGCC GGGTCGGCGC GACGGGGTTC
1801 TCGGACAACC TGTGCGCTGC GTCGGTCGTC ATCATCTTCT
25 CAAACTCCGG GACTGAAGAA GTGATCCGGG GACGGGAGAC
GTTTGAAGCT TGAATGACTG AGACTGAAAG TGAAGGCGCA
GCAGAGGCAG GCAGCATTAG TAGTAAGTAG TAAGTAAGTA
GCAGTGGAAC AAAGTAATAG TCGTTCGTTT TTCCCTGTGTA
2001 ATAAATAAGA GGCTGTGTGT TGAGGTAAAA AAAAAAA
30

In the event that this sequence contains an error, see the corresponding sequence in the accompanying figures.

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(2b) INFORMATION FOR SEQUENCE I.D. 2

SEQUENCE TYPE: NUCLEIC ACID
MOLECULE TYPE: DNA
5 ORIGINAL SOURCE: BARLEY
SEQUENCE LENGTH: 1822
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
10 SEQUENCE: Nucleotide sequence of a cDNA encoding the small
subunit of ADP-glucose pyrophosphorylase from barley
seed endosperm (beps)
COMMENT: The "." at 1569 denotes a purine.

SEQ. ID. No. 2

15
1 AAAAGTGAAC TCACACATCA CTCAATATCT ATATCCTTCC
ATTTTATATC CCTCGGTGAT GGATGTACCT TTGGCATCTA
AAGTTCCTT GCCCTCCCCT TCCAAGCATG AACAAATGCAA
CGTTTATAGT CATAAGAGCT CATCGAAGCA TGCAGATCTC
20 AATCCCCATG CTATTGATAG TGTTCTCGGT ATCATTCTTG
201 GAGGTGGTGC AGGGACTAGA TTGTATCCCC TGACGAAGAA
GCGTGCAAAG CCTGCAGTGC CATTGGGTGC CAACTACAGG
CTTATTGATA TTCCTGTCAG TAATTGTCTG AACAGCAACA
TATCAAAGAT CTATGTGCTT ACACAGTTCA ACTCAGCTTC
25 TCTTAATCGT CATCTCTCAC GAGCCTATGG GAGCAACATT
401 GGAGGTTACA AGAATGAAGG ATTTGTTGAA GTCCTTGCTG
CACAGCAGAG CCCAGATAAC CCTGACTGGT TCCAGGGTAC
TGCAGATGCT GTAAGGCAGT ACTTGTGGCT ATTCGAGGAG
CATAATGTTA TGGAGTATCT AATTCTTGCT GGAGATCACC
30 TGTACCGAAT GGAATATGAA AAGTTTATTC AGGCACACAG
601 AGAAACGGAT GCTGATATTA CTGTTGCTGC CTGCCCATG
GATGAGGAAC GTGCAACTGC ATTTGGCCTT ATGAAAATCG
ATGAAGAAGG GAGGATAATT GAATTCCGAG AGAAACCAAA
AGGAGAACAG TTGAAAGCTA TGATGGTTGA TACGACCATA
35 CTTGGCCTTG AAGATGCGAG GGCAAAGGAA ATGCCTTATA
801 TTGCTAGCAT GGGTATCTAT GTTATTAGCA AACATGTGAT
GCTTCAGCTT CTCCGTGAGC AATTCCTGG AGCTAATGAC
TTCGGAAGTG AAGTTATCCC TGGTGCAACT AGCACTGGCA
TGAGGGTACA AGCATACCTA TACGACGGTT ACTGGGAAGA
40 TATTGGTACA ATTGAGGCAT TCTATAATGC AAATTTGGGA
1001 ATTACCAAAA AACCAATACC TGATTTCAGT TTCTATGACC
GTTCTGCTCC CATTTACACA CAACCTCGAC ACTTGCCTCC
TTCAAAGGTT CTTGATGCTG ATGTGACAGA CAGTGTAATT
GGTGAAGGAT GTGTTATTAA AAAGTGAAG ATACACCATT
45 CAGTAGTTGG ACTCCGTTCC TGCATATCTG AAGGTGCAAT
1201 AATAGAGGAC ACGTTGCTAA TGGGTGCGGA CTACTATGAG
ACTGAAGCTG ATAAGAAACT CTTGCTGAA AAAGGTGGCA
TTCCCATTTG TATTGGAAAG AATTCACACA TCAAAGAGC

- 40 -

AATCATTGAC AAGAATGCTC GTATTGGAGA TAACGTGATG
ATAATCAATG TTGACAATGT TCAAGAAGCG GCGAGGGAGA
1401 CAGATGGATA CTTCATCAAA AGTGGCATCG TAACTGTGAT
CAAGGATGCT TTACTIONCTA GTGGAACAGT CATATGAAGC
5 AGATGTGAAA TGTATGCCAA AAGACAGGGC TACTTGCGTC
AGTCTGGAAT CAACCAACAA GGCCGCGAAG GAGATCATAA
AATAAAAA.G GAGTGCCATG CGAGTCACTT CTACACCCTT
1601 TTCCCCCCTT GATGTATTAG GAACTGTGAT GTACAAGCAA
CTGTGATGCA CTTACGCGAA GTGCCCCTGG ATTCAGCTTT
10 CTCTTTGCTT GTAACCTGGTT TCCAGCAGAC CATGCTATTT
GTTGTATGGT TCGTGCAAAA CCTTGCGATG CTTTATATAT
GCTTTATATA TAAACAAGAT GAATCCCCGC GCGTTGCTGC
2001 GGCACAAAAA AAAAAAAAAA AA

15

20 In the event that this sequence contains an error, see the corresponding sequence in
the accompanying figures.

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(2c) INFORMATION FOR SEQUENCE I.D. 3

SEQUENCE TYPE: ENZYME
 MOLECULE TYPE: AMINO ACID
 5 ORIGINAL SOURCE: BARLEY
 SEQUENCE LENGTH: 528
 TOPOLOGY: LINEAR
 SEQUENCE: Derived amino acid sequence of a cDNA encoding the
 large subunit of ADP-glucose pyrophosphorylase from
 10 barley seed endosperm (bep110)

SEQ. ID. No. 3

1	M S S M Q F S S V L	P L E G K A C V S P
15	V R R E G S A C E R	L K I G D S S S I R
	H E R A S R R M C N	G G A G A P P P P V
	R S A C S P P T P A	R P T P L F S G R P
	S G G I T P I R T R	S R P S V A A V I L
101	G G G T G T Q L F P	L T S T R A T P A V
20	P I G G C Y R L I D	I P M S N C F N S G
	I N K I F V M T Q F	N S A S L N R H I H
	R T Y L G G G I N F	T D G S V E V L A A
	T Q M P G E A A G W	F R G T A D A V R K
201	F I W V L E D Y Y K	H K S I E H I L I L
25	S G D Q L Y R M D Y	M E L V Q K H V D D
	N A D I T L S C A P	V G E S R A S E Y G
	L V K F D S S G R V	I Q F S E K P K G D
	D L E A M K V D T S	F L N F A I D D P A
301	K Y P Y I A S M G V	Y V F K R D V L L N
30	L L K S R Y A E L H	D F G S E I L P R A
	L H D H N V Q A Y V	F T D Y W E D I G T
	I R S F F D A N M A	L C E Q P P K F E F
	Y D P K T P F F T S	P R Y L P P T K S D
401	K C R I K E A I I S	H G C F L R E C K I
35	E H S I I G V R S R	L N S G S E L K N A
	M M M G A D S Y E T	E D E I S R L M S E
	G K V P I G V G E N	T K I S N C I I D M
	N A R I G R D V V I	S N K E G V Q E A D
501	R P E E G Y Y I R S	G I V V I Q K N A T
40	I K D G T V V *	

In the event that this sequence contains an error, see the corresponding sequence in the accompanying figures.

45

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(2d) INFORMATION FOR SEQUENCE I.D. 4

SEQUENCE TYPE: ENZYME
 MOLECULE TYPE: AMINO ACID
 5 ORIGINAL SOURCE: BARLEY
 SEQUENCE LENGTH: 472
 TOPOLOGY: LINEAR
 SEQUENCE: Derived amino acid sequence of a cDNA encoding the
 10 small subunit of ADP-glucose pyrophosphorylase from
 barley seed endosperm (beps)

SEQ. ID. No. 4

15	1	D V P L A S K V P L	P S P S K H E Q C N
		V Y S H K S S S K H	A D L N P H A I D S
		V L G I I L G G G A	G T R L Y P L T K K
		R A K P A V P L G A	N Y R L I D I P V S
		N C L N S N I S K I	Y V L T Q F N S A S
20	101	L N R H L S R A Y G	S N I G G Y K N E G
		F V E V L A A Q Q S	P D N P D W F Q G T
		A D A V R Q Y L W L	F E E H N V M E Y L
		I L A G D H L Y R M	D Y E K F I Q A H R
		E T D A D I T V A A	L P M D E E R A T A
25	201	F G L M K I D E E G	R I I E F A E K P K
		G E Q L K A M M V D	T T I L G L E D A R
		A K E M P Y I A S M	G I Y V I S K H V M
		L Q L L R E Q F P G	A N D F G S E V X P
		G A T S T G M R V Q	A Y L Y D G Y W E D
30	301	I G T I E A F Y N A	N L G I T K K P I P
		D F S F Y D R S A P	I Y T Q P R H L P P
		S K V L D A D V T D	S V I G E G C V I K
		N C K I H H S V V G	L R S C I S E G A I
		I E D T L L M G A D	Y Y E T E A D K K L
35	401	L A E K G G I P I G	I G K N S H I K R A
		I I D K N A R I G D	N V M I I N V D N V
		Q E A A R E T D G Y	F I K S G I V T V I
		K D A L L P S G T V	I *

40

In the event that this sequence contains an error, see the corresponding sequence in the accompanying figures.

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(2e) INFORMATION FOR SEQUENCE I.D. 5

	SEQUENCE TYPE:	NUCLEIC ACID
	MOLECULE TYPE:	DNA
5	ORIGINAL SOURCE:	POTATO
	SEQUENCE LENGTH:	480
	STRANDEDNESS:	DOUBLE
	TOPOLOGY:	LINEAR
10	SEQUENCE:	Starch branching enzyme cDNA (First 480 nucleotides from 5' end)

SEQ. ID. No. 5

```
1   CCCGTCTGTA AGCATCATTA GTGATGTTGT
15  31   TCCAGCTGAA TGGGATGATT CAGATGCAAA
    61   CGTCTGGGGT GAGAACATAC AAGAAGGCAG
20  91   CAGCTGAAGC AAAGTACCAT AATTTAATCA
    121  ATGGAAATTA ATTTCAAAGT TTTATCAAAA
    151  CCCATTCGAG GATCTTTTCC ATCTTTCTCA
25      CCTAAAGTTT CTTCAGGGGC TTCTAGAAAT
      AAGATATGTT TTCCTTCTCA ACATAGTACT
30      GGACTGAAGT TTGGATCTCA GGAACGGTCT
      TGGGATATTT CTTCCACCCC AAAATCAAGA
    301  GTTAGAAAAG ATGAAAGGAT GAAGCACAGT
35      TCAGCTATTT CCGCTGTTTT GACCGATGAC
      AATTCGACAA TGGCACCCCT AGAGGAAGAT
40      GTCAAGACTG AAAATATTGG CCTCCTAAAT
      TTGGATCCAA CTTTGGAACC TTATCTAGAT
    451  CACTTCAGAC ACAGAATGAA GAGATATGTG
45
```

In the event that this sequence contains an error, see the corresponding sequence in the accompanying figures.

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(2f) INFORMATION FOR SEQUENCE I.D. 6

SEQUENCE TYPE: PEPTIDE
 MOLECULE TYPE: AMINO ACID
 5 ORIGINAL SOURCE: POTATO
 SEQUENCE LENGTH: 120
 TOPOLOGY: LINEAR
 SEQUENCE: Starch branching enzyme amino acid
 (First 120 amino acids from amino terminus)

10

SEQ. ID. No. 6

1 MET Glu Ile Asn Phe Lys Val Leu Ser Lys
 15 11 Pro Ile Arg Gly Ser Phe Pro Ser Phe Ser
 21 Pro Lys Val Ser Ser Gly Ala Ser Arg Asn
 20 31 Lys Ile Cys Phe Pro Ser Gln His Ser Thr
 41 Gly Leu Lys Phe Gly Ser Gln Glu Arg Ser
 51 Trp Asp Ile Ser Ser Thr Pro Lys Ser Arg
 25 61 Val Arg Lys Asp Glu Arg MET Lys His Ser
 71 Ser Ala Ile S er Ala Val Leu Thr Asp Asp
 30 81 Asn Ser Thr MET Ala Pro Leu Glu Glu Asp
 91 Val Lys Thr Glu Asn Ile Gly Leu Leu Asn
 101 Leu Asp Pro Thr Leu Glu Pro Tyr Leu Asp
 35 111 His Phe Arg His Arg MET Lys Arg Tyr Val

40 In the event that this sequence contains an error, see the corresponding sequence in the accompanying figures.

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(2g) INFORMATION FOR SEQUENCE I.D. 7

SEQUENCE TYPE: NUCLEIC ACID
MOLECULE TYPE: DNA
5 ORIGINAL SOURCE: POTATO
SEQUENCE LENGTH: 1047
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
SEQUENCE: Tuber specific class 1 promoter

10

SEQ. ID. No. 7

1 TTGTTAGTTA ATGCGTATTA GTTTTAGCGA CGAAGCACTA
AATCGTCTTT GTATACTTTC AGTGACACAT GTTAGTGAC
15 GACTGATTGA CGAAATTTT TTCGTCTCAC AAAATTTTTA
GTGACGAAAC ATGATTTTATA GATGACGAAA TTATTTGTCC
CTCATAATCT AATTTGTTGT AGTGATCATT ACTCCTTTGT
201 TTGTTTTATT TGTCATGTTA GTTCATTAAA AAAAAAATCT
CTCTTCTTAT CAATTCTGAC GTGTTTAATA TCATAAGATT
20 AAAAAATATT TTAATATATC TTTAATTTAA AGCCACAAAA
TTTAAATTTT TTCGTTAACA TAATTTGTCA AATCAGGCTC
AAAGATCGTT TTTCATATCG GAATCAGGAT TTTATTTATT
401 CTTTTAAAAA TAAAGAGGTG GTGAGCTAAA CAATTTCAAA
TCTCATCACA CATATGGGGT CAGCCACAAA AATAAAGAAC
25 GGTGGAACG GATCTATTAT ATAATACTAA TAAAGAATAG
AAAAAGGAAA GTGAGTGAGG TGCGAGGGAG AGAATCTGTT
TAATATGCAG AGTCGATCAT GTGTCAGTTT TATCGATATG
601 ACTCTGATTT CAACTGAGTT TAAGCAATTC TGATAAGGCG
AGGAAAATCA CAGTGCTGAA ATCTAGAAAA ATCTCATACA
30 GTGAGATAAA TCTCAACAAA AACGTTGAGT CCATAGAGGG
GGTGTATGTG ACACCCAACC TCAGCAAAAG AAAACCTCCC
CTCAAGAAGG ACATTTGCGG TGCTAAACAA TTTCAAGTCT
801 CATCACACAT ATATATTATA TAATACTAAT AAAGAATAGA
AAAAGGAAAG GTAAACATCA CTAATGACAG TTGCGGTGCA
35 AAGTGAGTGA GATAATAAAC ATCAGTAATA GACATCACTA
ACTTTTATTG GTTATGTCIT TCTCAAAATA AAATTTCTCA
ACTTGTTTAC GTGCCTATAT ATACCATGCT TGTTATATGC
1001 TCAAAGCACC AACAAAATTT AAAAACACTT TGAACATTTG
CCCCGGG

40

45

In the event that this sequence contains an error, see the corresponding sequence in the accompanying figures.

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(2h) INFORMATION FOR SEQUENCE I.D. 8

SEQUENCE TYPE: ENZYME CONSTRUCT
MOLECULE TYPE: AMINO ACID
5 ORIGINAL SOURCE: SPINACH and BARLEY
SEQUENCE LENGTH: 120
TOPOLOGY: LINEAR
SEQUENCE: Amino terminal amino acid sequence of the rubisco
10 activase - AGP small subunit fusion enzyme.

SEQ.ID.NO.8

1 MATAVSTVGA ATRAPLNNG SSAGASVPTS GFLGSSLKKH 40
15 41 TNVRFPSRR TTSMTVKAAE NEEKNTDKWA HLAKDFSDDQ 80
81 LDIRRGKGMV DSLGSMDVPL ASKVPLPSPS KHEQCNVYSH 120

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(2i) INFORMATION FOR SEQUENCE I.D. 9

SEQUENCE TYPE: ENZYME CONSTRUCT
MOLECULE TYPE: AMINO ACID
5 ORIGINAL SOURCE: SPINACH and BARLEY
SEQUENCE LENGTH: 120
TOPOLOGY: LINEAR
SEQUENCE: Amino terminal amino acid sequence of the rubisco
10 activase - AGP large subunit fusion enzyme.

SEQ.ID.NO.9

1 MATAVSTVGA ATRAPLNLNG SSAGASVPTS GFLGSSLKKH 40
15 41 TNVRFPSRR TTSMTVKAAE NEEKNTDKWA HLAKDFSDDQ 80
81 LDIRRGKGMV DSLGIHMQFS SVLPLEGKAC VSPVRREGSA 120

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(2j) INFORMATION FOR SEQUENCE I.D. 10

SEQUENCE TYPE: ENZYME CONSTRUCT
MOLECULE TYPE: AMINO ACID
5 ORIGINAL SOURCE: SPINACH and BARLEY
SEQUENCE LENGTH: 120
TOPOLOGY: LINEAR
SEQUENCE: Amino terminal amino acid sequence of the starch
branching enzyme - AGP large subunit fusion enzyme.
10

SEQ.ID.NO.10

1 MEINFKVL SK PIRGSFPSFS PKVSSGASRN KICFPSQHST 40
15 41 GLKFGSQERS WDISSTPKSR VRKDERMKHS SAISAVLTDD 80
81 NSTMAPLEED VKTENIGLLN LDPMQFSSVL PLEGKACVSP 120

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>19</u> , line <u>6</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23. St. Machar Drive Aberdeen Scotland United Kingdom AB2 1RY	
Date of deposit 29 March 1994	Accession Number NCIMB 40618
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect of those designations in which a European patent is sought, and any other designated state having equivalent legislation, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample. (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<p style="text-align: center;">For receiving Office use only</p> <p><input checked="" type="checkbox"/> This sheet was received with the international application</p> <hr/> <p>Authorized officer</p> <p style="text-align: center;"><i>R.L.R.</i> R.L.R. PETHER</p>	<p style="text-align: center;">For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <hr/> <p>Authorized officer</p>
---	--

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)


A. The indications made below relate to the microorganism referred to in the description on page <u>19</u> , line <u>8</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23. St. Machar Drive Aberdeen Scotland United Kingdom AB2 1RY	
Date of deposit 29 March 1994	Accession Number NCIMB 40619
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect of those designations in which a European patent is sought, and any other designated state having equivalent legislation, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample. (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application Authorized officer <u>R.L.R.</u> R.L.R. PETHER	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer _____
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>19</u> , line <u>10</u>	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23. St. Machar Drive Aberdeen Scotland United Kingdom AB2 1RY	
Date of deposit 29 March 1994	Accession Number NCIMB 40620
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect of those designations in which a European patent is sought, and any other designated state having equivalent legislation, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample. (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only	
<input checked="" type="checkbox"/> This sheet was received with the international application	
Authorized officer <div style="text-align: center;">  R.L.R. PETHER </div>	

For International Bureau use only	
<input type="checkbox"/> This sheet was received by the International Bureau on:	
Authorized officer	

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>19</u> , line <u>12</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23. St. Machar Drive Aberdeen Scotland United Kingdom AB2 1RY	
Date of deposit 29 March 1994	Accession Number NCIMB 40621
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect of those designations in which a European patent is sought, and any other designated state having equivalent legislation, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample. (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>19</u> , line <u>14</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
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Address of depositary institution (including postal code and country) 23. St. Machar Drive Aberdeen Scotland United Kingdom AB2 1RY	
Date of deposit 29 March 1994	Accession Number NCIMB 40622
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D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>19</u> , line <u>21</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23. St. Machar Drive Aberdeen Scotland United Kingdom AB2 1RY	
Date of deposit 31 March 1994	Accession Number NCIMB 40623
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In respect of those designations in which a European patent is sought, and any other designated state having equivalent legislation, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample. (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; justify-content: space-between; align-items: flex-start;"> <div style="width: 40%;"> <input checked="" type="checkbox"/> This sheet was received with the international application </div> <div style="width: 50%; text-align: center;"> <div style="margin-bottom: 20px;">Authorized officer</div> <div style="font-family: cursive; font-size: 1.2em;">R.L.R.</div> <div>R.L.R. PETHER</div> </div> </div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; justify-content: space-between; align-items: flex-start;"> <div style="width: 40%;"> <input type="checkbox"/> This sheet was received by the International Bureau on: </div> <div style="width: 50%; text-align: center;"> <div style="margin-bottom: 20px;">Authorized officer</div> <div style="height: 40px;"></div> </div> </div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>19</u> , line <u>23</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23. St. Machar Drive Aberdeen Scotland United Kingdom AB2 1RY	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>19</u> , line <u>25</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution The National Collections of Industrial and Marine Bacteria Limited (NCIMB)	
Address of depositary institution (including postal code and country) 23. St. Machar Drive Aberdeen Scotland United Kingdom AB2 1RY	
Date of deposit 31 March 1994	Accession Number NCIMB 40625
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect of those designations in which a European patent is sought, and any other designated state having equivalent legislation, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample. (Rule 28(4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
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CLAIMS

1. A transgenic starch producing organism comprising a nucleotide sequence coding for an exogenous ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof which retains the enzymatic activity of the AGP enzyme, wherein the nucleotide sequence is capable of being expressed in the organism;

characterised in that the activity of the enzyme or sub-unit thereof is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate; and

further characterised in that the activity of the enzyme or sub-unit thereof is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

2. An organism according to claim 1 wherein the AGP enzyme is a heteromer, preferably a heterotetramer, more preferably a heteromer containing two large sub-units and two small sub-units.

3. An organism according to claim 2 wherein the AGP enzyme is isolatable from Hordeum, preferably wherein the enzyme is barley (Hordeum vulgare) endosperm AGP or a sub-unit thereof, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequences defining the barley endosperm AGP or either of its sub-units.

4. An organism according to claim 3 wherein the nucleotide sequence is a DNA sequence.

5. An organism according to claim 4 wherein the DNA sequence encodes the large sub-unit of the barley endosperm AGP or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequence defining the large sub-unit of the barley endosperm AGP.

6. An organism according to claim 4 or claim 5 wherein the DNA sequence is the sequence identified herein as SEQ ID No 1, including non-critical allelic variations of that sequence.
- 5 7. An organism according to claim 4 wherein the DNA sequence encodes the small sub-unit of the barley endosperm AGP, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequence defining the small sub-unit of the barley endosperm AGP.
- 10 8. An organism according to claim 4 or claim 7 wherein the DNA sequence is the sequence identified herein as SEQ ID No 2, including non-critical allelic variations of that sequence.
9. An organism according to claim 4 comprising a DNA sequence according to
15 claim 5 or claim 6 and a DNA sequence according to claim 7 or claim 8, preferably wherein each DNA sequence additionally codes for a different marker.
10. An organism according to any one of the preceding claims wherein the expressed AGP enzyme or sub-unit thereof comprises the amino acid sequence set out
20 in SEQ ID No. 3, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.
11. An organism according to any one of claims 1 to 9 wherein the expressed AGP enzyme or sub-unit thereof comprises the amino acid sequence set out in SEQ
25 ID No. 4, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.
12. An organism according to claim 1 wherein the expressed AGP comprises both a large sub-unit having the amino acid sequence set out in SEQ ID No. 3 or a variant
30 thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence, and a small sub-unit having the amino acid sequence set out in SEQ ID No. 4 or a variant thereof having non-critical amino acid

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substitution(s) or deletion(s) at one or more locations in that sequence.

13. An organism according to any one of the preceding claims wherein the nucleotide sequence additionally codes for a transit peptide.

5

14. An organism according to claim 13 wherein the transit peptide is Rubisco Activase transit peptide or Starch Branching enzyme transit peptide.

15. An organism according to claim 14 wherein the transit peptide is coded for by a DNA sequence comprising the sequence identified as SEQ. I.D. No. 5, including non-critical allelic variations of that sequence.

10

16. An organism according to claim 14 wherein the transit peptide has an amino acid sequence comprising the sequence identified as Seq.I.D.No. 6, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.

15

17. An organism according to claim 4 wherein the nucleotide sequence is operatively connected to a promoter which expresses the nucleotide sequence wherein the promoter is cell, tissue or organ specific.

20

18. An organism according to claim 17 wherein the promoter has the sequence identified as SEQ.I.D.No.7, or a variant thereof having non-critical nucleotide substitution(s) or deletion(s) at one or more locations in that sequence.

25

19. A transgenic starch producing organism comprising exogenous ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof which retains the enzymatic activity of the AGP enzyme, wherein the activity of the enzyme or sub-unit thereof is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate and wherein the activity of the enzyme or sub-unit thereof is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

30

- 60 -

20. An organism according to claim 19 wherein the AGP enzyme or sub-unit thereof comprises the amino acid sequence set out in SEQ ID No. 3, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence and/or the amino acid sequence set out in SEQ ID No. 4,
5 or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.

21. An organism according to any one of the preceding claims wherein the organism is a transgenic plant.

10

22. An organism according to claim 20 wherein the transgenic plant is a potato plant.

23. A potato tuber containing an enhanced starch content, when obtained from a
15 transgenic potato plant according to claim 22.

24. A method of increasing the rate and/or yield of starch production in an organism, especially a plant or a plant cell, which method comprises introducing into an organism a nucleotide sequence as defined in claim 1 or any claim dependent
20 thereon to form a transgenic organism as defined in any one of the preceding claims and expressing the nucleotide sequence.

25. A method of increasing the rate and/or yield of starch production in an organism, especially a plant or a plant cell, which method comprises introducing into
25 or forming in an organism a ADP glucose pyrophosphorylase (AGP) enzyme or a sub-unit thereof as defined in claim 19 or any claim dependent thereon.

26. A cDNA sequence identified herein as SEQ ID No. 2, including non-critical allelic variations of that sequence.

30

- 61 -

27. An amino acid sequence as shown in SEQ ID No. 4, including variants thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations in that sequence.
- 5 28. A cDNA sequence identified herein as SEQ ID No. 5 including non-critical allelic variations of that sequence.
29. An amino acid sequence as shown in SEQ ID No. 6, including variants thereof having non-critical amino acid substitution(s) or deletion(s) at one or more locations
10 in that sequence.
30. An AGP enzyme or sub-unit thereof whose *in vivo* activity is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate, and whose activity is not stimulated by fructose-1,6-bisP and/or
15 is not inhibited by AMP.
31. Plasmid pPPS1.
32. Plasmid pPPL1.
20
33. Plasmid pPPL1M.
34. Plasmid pPPS4.
- 25 35. Plasmid pPPL4.
36. Plasmid pPPL5.
37. Plasmid pBKL4.
30
38. Plasmid pVictor IV GN.

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39. A method of increasing the rate and/or yield of starch production in an organism, especially a plant or a plant cell, which method comprises introducing into an organism a recombinant DNA construct containing an exogenous DNA sequence encoding an exogenous ADP glucose pyrophosphorylase enzyme (AGP) or sub-unit thereof and one or more promoter sequences enabling the expression of the AGP encoded by that sequence by the organism thereby to increase the AGP content of the organism and in consequence to increase the rate of starch production by the organism and/or the starch yield, characterised in that the said DNA sequence is the gene sequence encoding the barley (Hordeum vulgare) endosperm AGP or a sub-unit thereof, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequences defining the barley endosperm AGP or either of its sub-units, wherein the construct is expressed in the organism; characterised in that the activity of the enzyme or sub-unit thereof is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate; and further characterised in that the activity of the enzyme or sub-unit thereof is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

40. A vector for the transformation of an organism, especially a plant or a plant cell, to increase the AGP content of such an organism consequently to increase the rate of starch production by such an organism, such vector comprising a recombinant DNA construct containing a DNA sequence encoding an exogenous ADP glucose pyrophosphorylase enzyme (AGP), such vector also incorporating the necessary promoter and other sequences enabling the expression of that exogenous AGP in an organism transformed by that vector, characterised in that the said DNA sequence is the gene sequence encoding the barley (Hordeum vulgare) endosperm AGP or a sub-unit thereof, or a variant thereof having non-critical amino acid substitution(s) or deletion(s) at one or more points in the amino acid sequences defining the barley endosperm AGP or either of its sub-units, wherein the construct is capable of being expressed in the organism; characterised in that the activity of the enzyme or sub-unit thereof is substantially independent of any level of *in vivo* 3-phospho-glycerate and/or any *in vivo* level of inorganic phosphate; and further characterised in that the activity

- 63 -

of the enzyme or sub-unit thereof is not stimulated by fructose-1,6-bisP and/or is not inhibited by AMP.

41. A method of targeting an exogenous protein to the amyloplast of plants or
5 plant cells which comprises introducing into the plant or plant cell a recombinant DNA construct containing a DNA sequence encoding a starch branching enzyme transit peptide and an exogenous DNA sequence encoding the exogenous protein; wherein the construct is capable of being expressed in the plant or plant cells.

10 42. A method according to claim 41, characterised in that said DNA sequence encoding the starch branching enzyme comprises the sequence identified as SEQ.ID.No.5.

15 43. A method according to claim 41, characterised in that said starch branching enzyme expressed in the plant or plant cell by said construct comprises the amino acid sequence identified as SEQ.ID. No. 6.

44. A foodstuff made from or comprising an organism according to claim 1 or any claim dependent thereon.

20

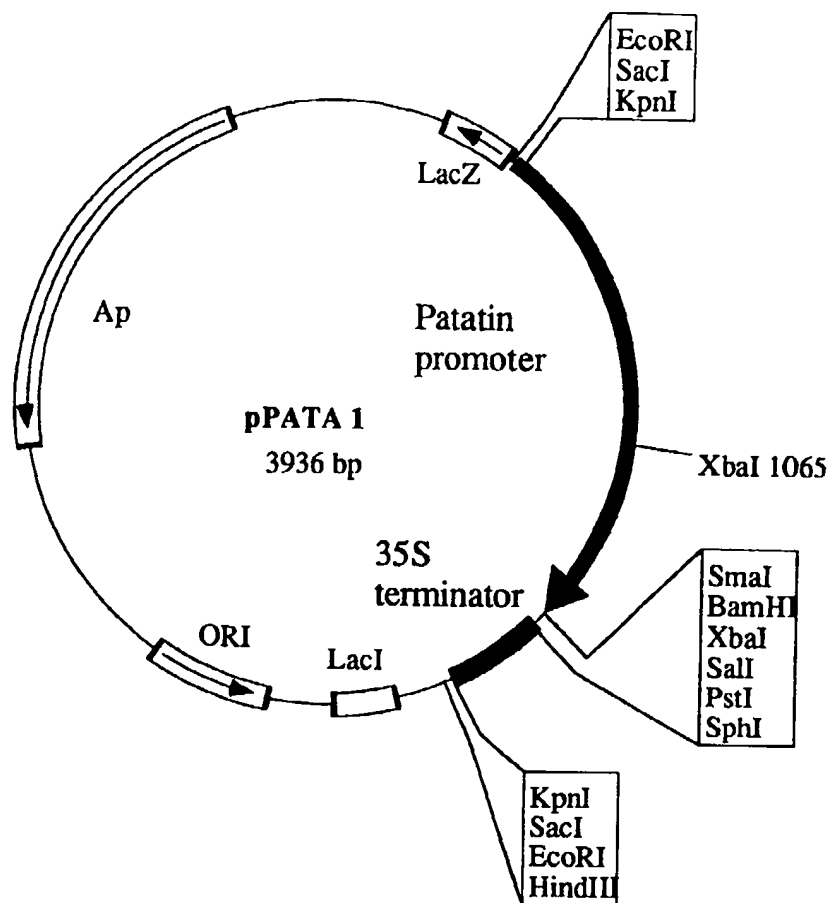
45. A foodstuff according to claim 44 wherein the foodstuff is a fried foodstuff.

46. A foodstuff according to claim 44 or claim 45 wherein the foodstuff is a potato.

25

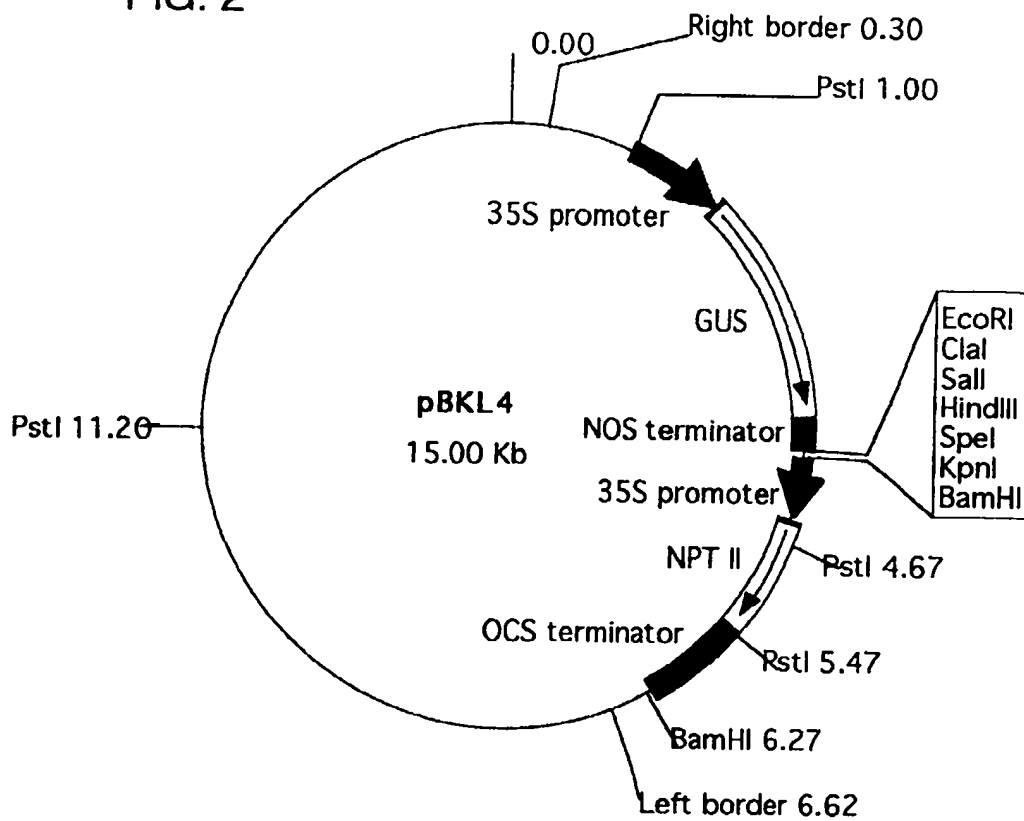
1/17

FIG. 1



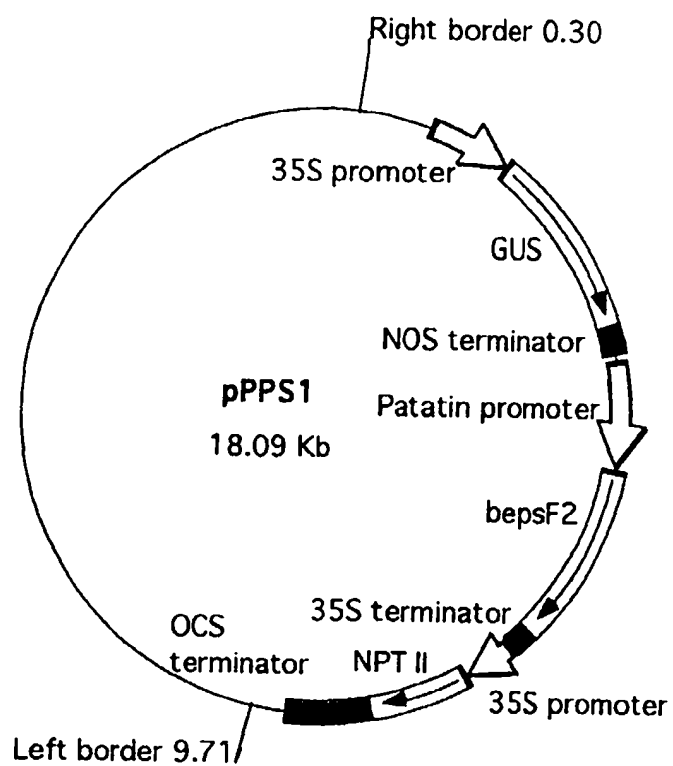
2/17

FIG. 2



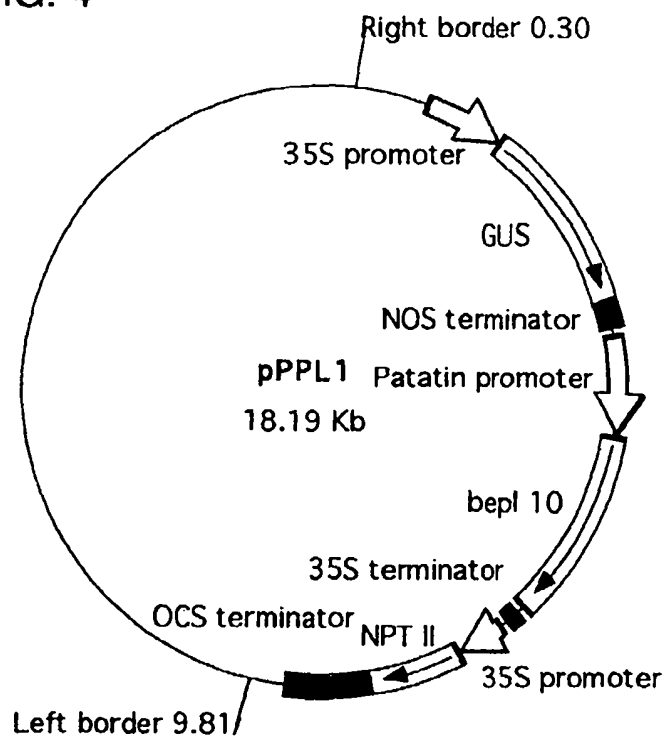
3/17

FIG. 3



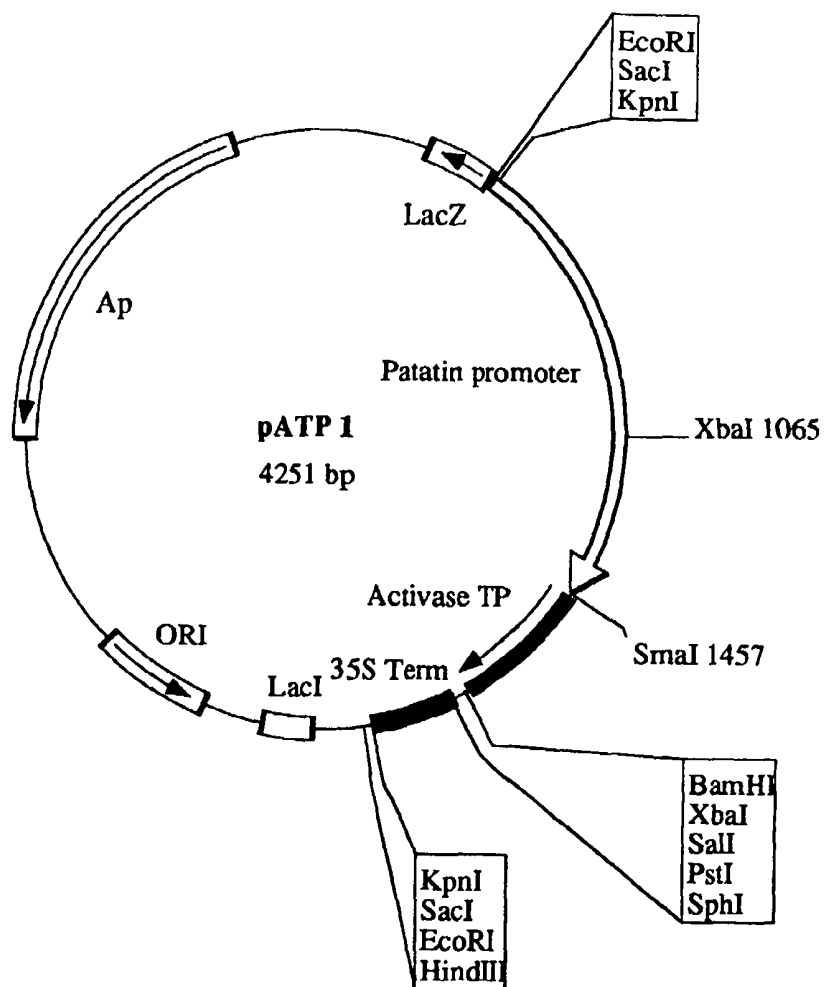
4/17

FIG. 4



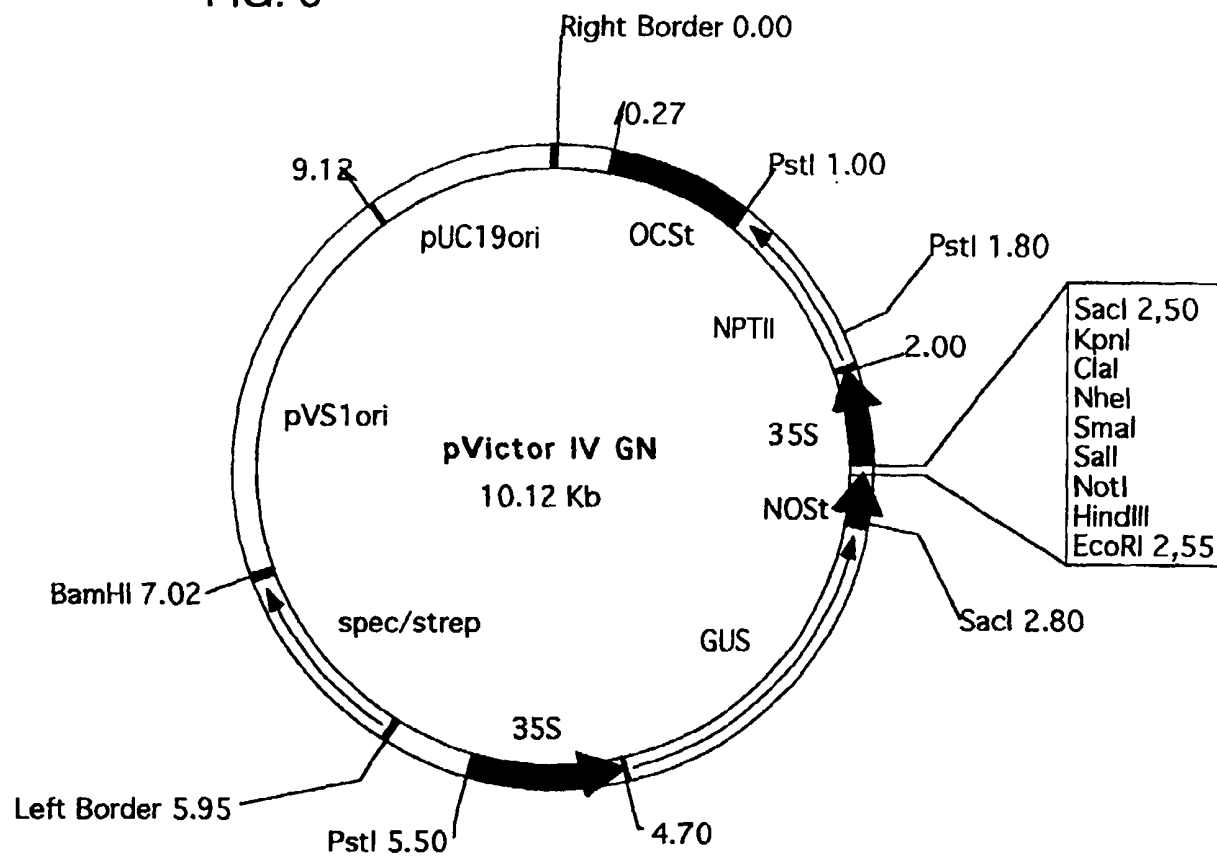
5/17

FIG. 5



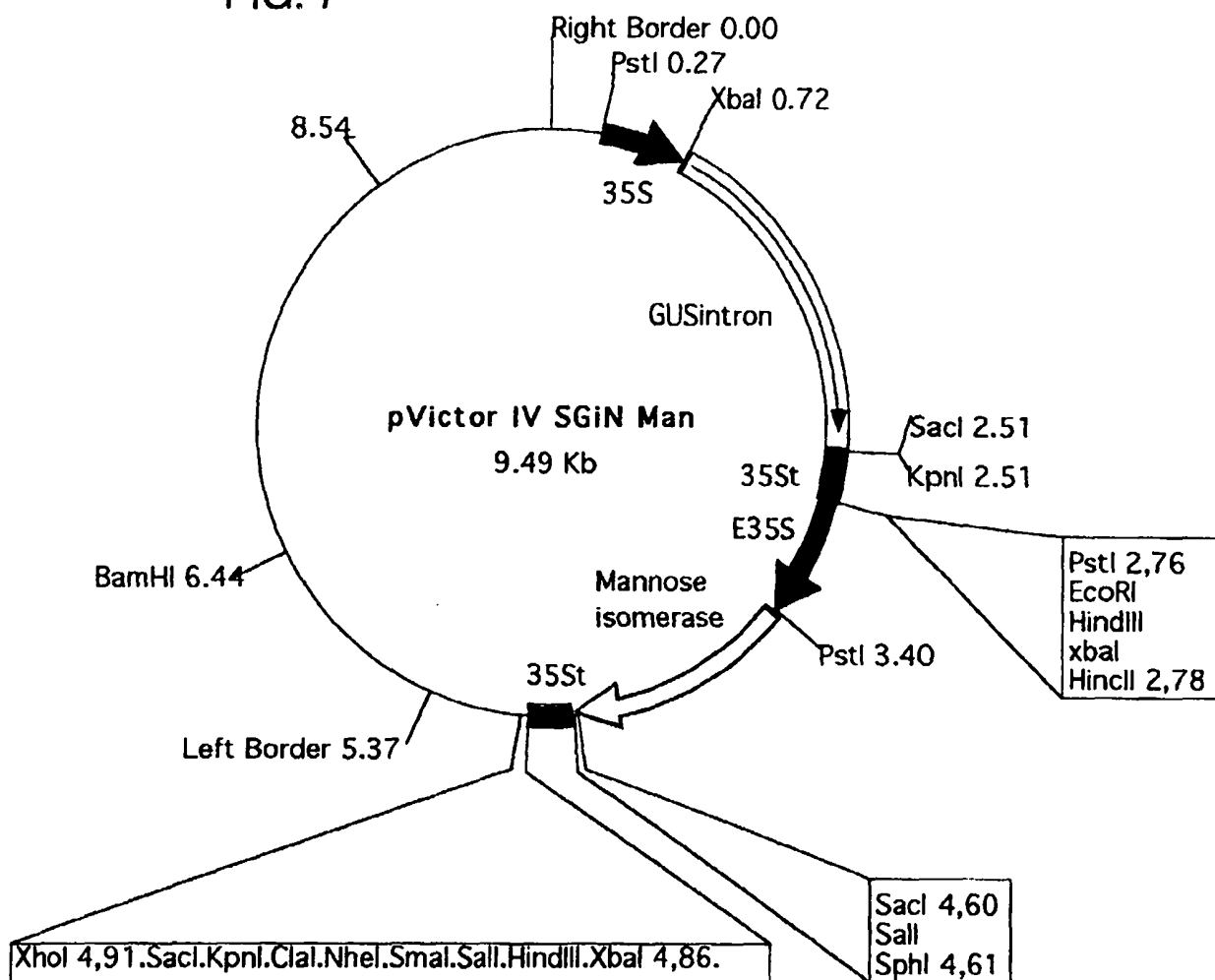
6/17

FIG. 6



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FIG. 7



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FIG 8

8.1 Amino terminal amino acid sequence of the rubisco activase - AGP small subunit fusion enzyme

1 MATAVSTVGA ATRAPLNLNG SSAGASVPTS GFLGSSLKKH 40
41 TNVRFPSRR TTSMTVKAAE NEEKNTDKWA HLAKDFSDDQ 80
81 LDIRRGKGMV DSLGSMDVPL ASKVPLSPS KHEQCNVYSH 120

8.2 Amino terminal amino acid sequence of the rubisco activase - AGP large subunit fusion enzyme

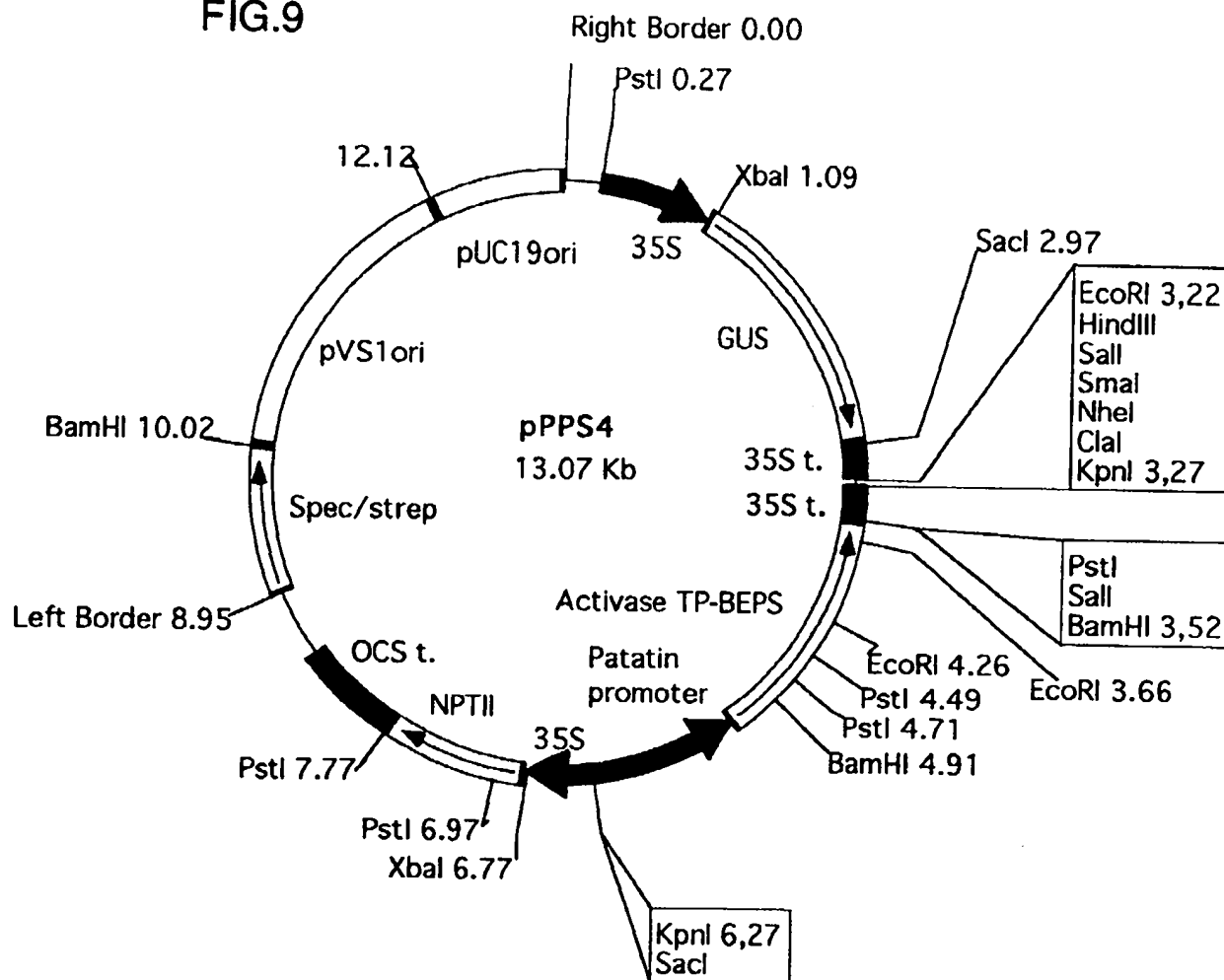
1 MATAVSTVGA ATRAPLNLNG SSAGASVPTS GFLGSSLKKH 40
41 TNVRFPSRR TTSMTVKAAE NEEKNTDKWA HLAKDFSDDQ 80
81 LDIRRGKGMV DSLGIHMQFS SVLPLEGKAC VSPVRREGSA 120

8.3 Amino terminal amino acid sequence of the starch branching enzyme - AGP large subunit fusion enzyme

1 MEINFKVLSK PIRGSFPSFS PKVSSGASRN KICFPSQHST 40
41 GLKFGSQERS WDISSTPKSR VRKDERMKHS SAISAVLTDD 80
81 NSTMAPLEED VKTENIGLLN LDPMQFSSVL PLEGKACVSP 120

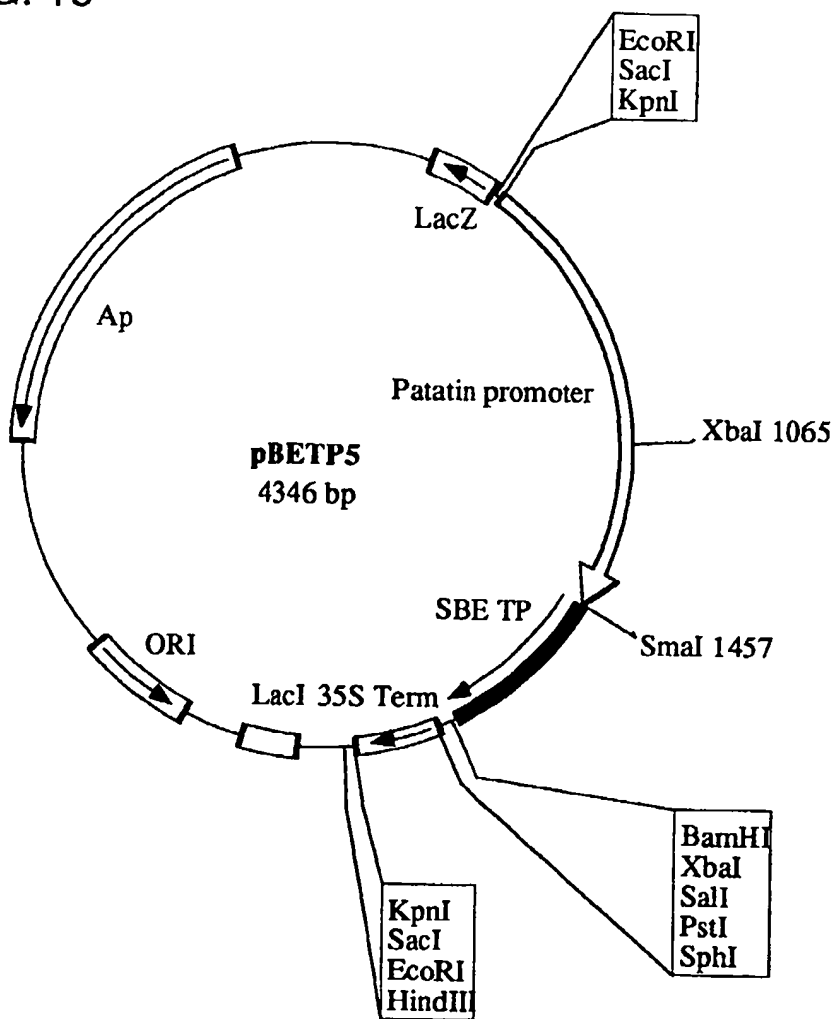
9/17

FIG.9



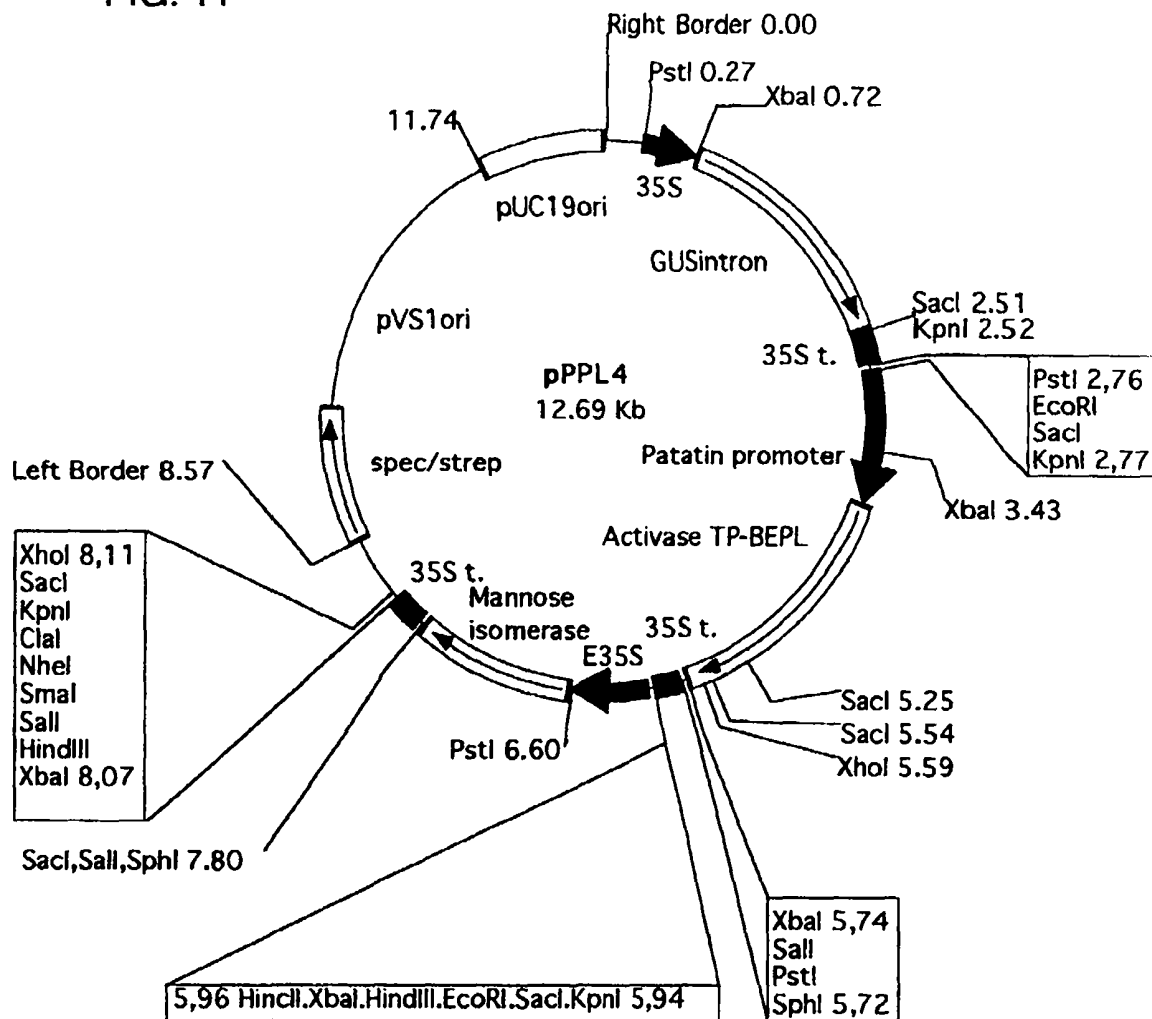
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FIG. 10



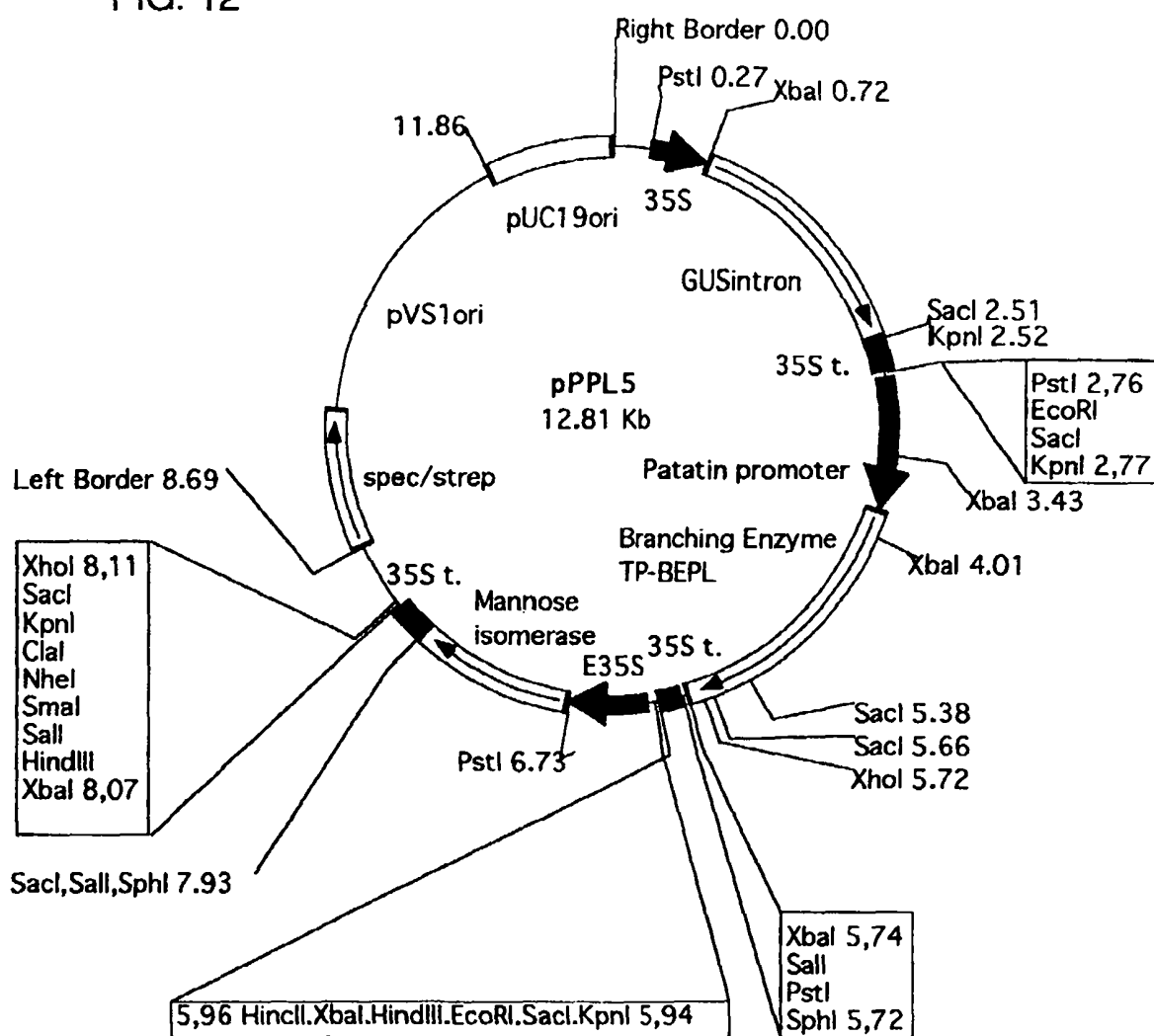
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FIG. 11



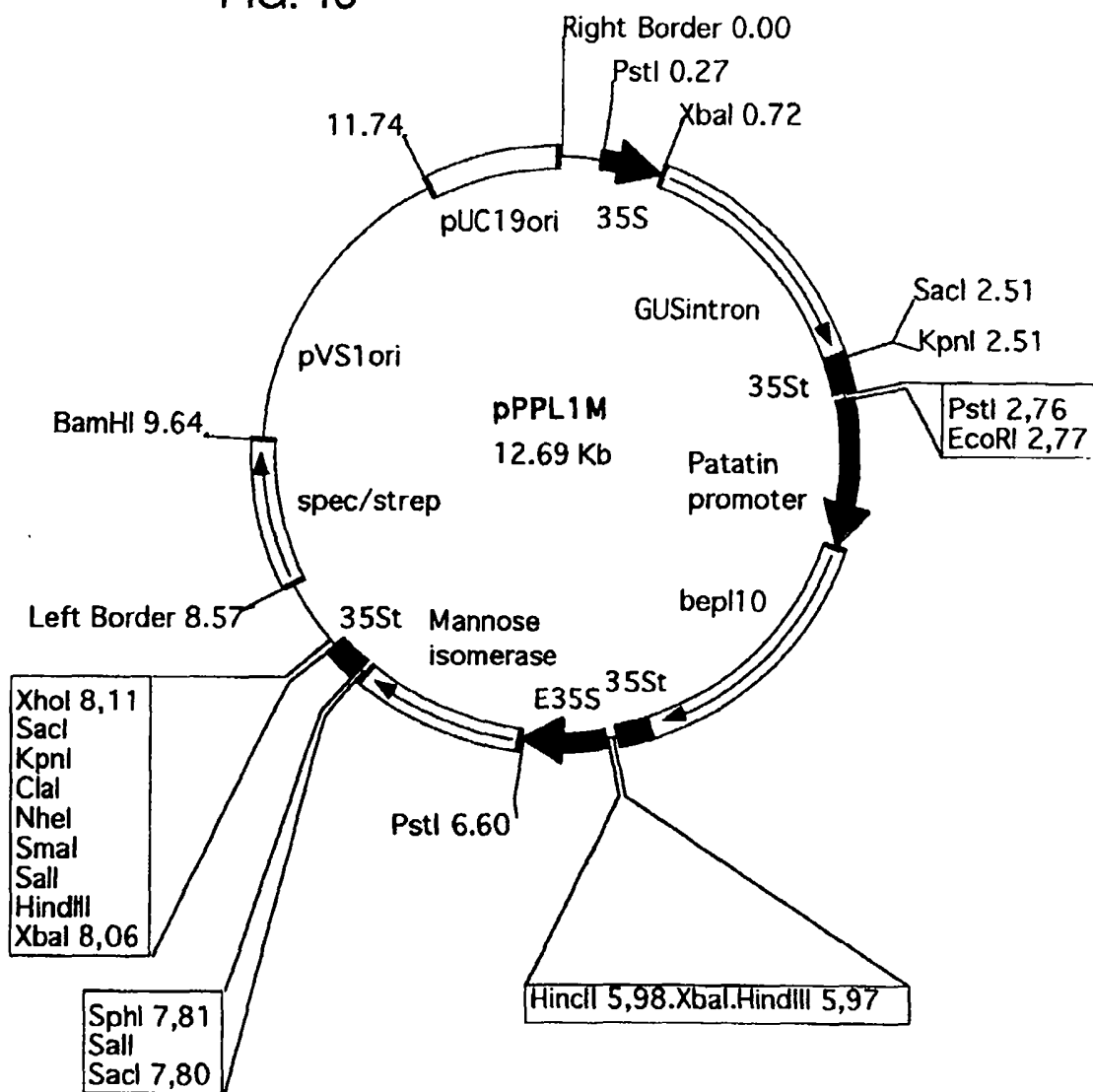
12/17

FIG. 12



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FIG. 13



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FIG. 14

Nucleotide sequence and derived amino acid sequence of a cDNA encoding the large subunit of ADP-glucose pyrophosphorylase from barley seed endosperm.

```

      10              30              50
ACGACCACCTCCGAACCTCAACGGCTCCACGGACCATCTCTCTCTCTCTCCCTCCCTTCAC

      70              90             110
CACCACCAACCAACCAACCCCTTCTCCCTCCCTGCATTGTGATTGTTTCATATTCATCCGT

     130             150             170
CGCTTGCCCGGTGGCCACCCCGTGGATCCCTCACCCTCGCCGTCCCGGCAGTTGCAGGTG

     190             210             230
GACTGCTAATGTTCATCGATGCAGTTCAGCAGGTGCTGCCCTGGAGGGCAAGGGGTGGC
      M S S M Q F S S V L P L E G K A C V

     250             270             290
TTTCCCCAGTTCAGGAGAGAGGGATCGGCTGGAGGGCTCAAGATCGGGGACAGCAGCA
      S P V R R E G S A C E R L K I G D S S S

     310             330             350
GCATCAGGCAACGAGAGAGCGTCCAGGAGGTGTGCAACGGCGGGCGAGGGGCCCCGGCCG
      I R H E R A S R R M C N G G A G A P P P

     370             390             410
CACCGGTGGCGAGTGGGTGCTCACCTCCGACGGCAGCCCGGGCGACACCTTGTTCCTCG
      P V R S A C S P P T P A R P T P L F S G

     430             450             470
GACGTCTTCCGGAGGAATTACGGCGATCCGAACGAGGTCCGGCGCGTGGTGGCGCCCG
      R P S G G I T P I R T R S R P S V A A V

     490             510             530
TCATACTCGGGCGGGCACCGGGACTCAGCTCTTCCCGCTCACAAGCACAGGGGCCACAC
      I L G G G T G T Q L F P L T S T R A T P

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550 570 590
CTGCTGTTCCATATGGAGGAATGTACAGGCTCATCGATATTCOCATGAGCAACTGCTTCA
A V P I G G C Y R L I D I P M S N C F N

610 630 650
ACAGTGGCATCAACAAGATATTGTCATGACCCAGTTCAACTCGGCATCTCTCAATGGCC
S G I N K I F V M T Q F N S A S L N R H

670 690 710
ACATTCAOCCCACTACCTCGGCGGGGAATCAATTTCACTGATGGATCTGTTGAGGTAT
I H R T Y L G G G I N F T D G S V E V L

730 750 770
TGCCCGGACACAAATGCCTGGGGAGGCTGCTGGATGGTTCCGCGGAACAGCGGATGCCG
A A T Q M P G E A A G W F R G T A D A V

790 810 830
TCAGAAAATTTATCTGGGTGCTTGAGGACTACTATAAGCATAAATCCATAGAGCACATTT
R K F I W V L E D Y Y K H K S I E H I L

850 870 890
TGATCTTGTCGGGCGATCAGCTTTATCGCATGGATTACATGGAGCTTGTCAGAAACATG
I L S G D Q L Y R M D Y M E L V Q K H V

910 930 950
TGATGACAATGCTGACATTACTTTATCATGTGCCCCCTGTTGGAGAGAGCCGGGCATCTG
D D N A D I T L S C A P V G E S R A S E

970 990 1010
AGTACGGGCTAGTGAAGTTGACAGTTCAGGCGGTGTGATCCAGTTTCTGAGAAGCCAA
Y G L V K F D S S G R V I Q F S E K P K

1030 1050 1070
AGGCGGACGATCTGGAAGCGATGAAAGTGGATACCAGTTTCTCAATTTGGCCATAGACG
G D D L E A M K V D T S F L N F A I D D

1090 1110 1130
ACCTGCTAAATATCCATACATTGCTTCGATGGGAGTTTATGTCTTCAAGAGCATGTTC
P A K Y P Y I A S M G V Y V F K R D V L

14b/17

1150 1170 1190
TGCTGAACTTCTTAAAGTCAAGATACGCAGAACTACATGACTTTGGGTCTGAAATCCTCC
L N L L K S R Y A E L H D F G S E I L P

1210 1230 1250
CGAGAGCTCTGCATGATCACAATGTACAGGCATATGTCTTCACTGACTACTGGCAGGACA
R A L H D H N V Q A Y V F T D Y W E D I

1270 1290 1310
TTGGAACAATCAGATCCTTCTTCGATCGGAACATGGCCCTCTGCGAACAGCCTCCAAAGT
G T I R S F F D A N M A L C E Q P P K F

1330 1350 1370
TTGAATTTTATGATCCAAAAACCCCTTCTTCACTTGGCTCGGTACTTACCGCCAACAA
E F Y D P K T P F F T S P R Y L P P T K

1390 1410 1430
AGTCAGACAAGTGCAGGATCAAGAAGCGATCATTTCGCACGGCTGCTTCTTGGGTGAAT
S D K C R I K E A I I S H G C F L R E C

1450 1470 1490
GCAAAATCGAGCACTCCATCATCGGCGTTGGTTACCGCTTAACTCCGGAAGCGAGCTCA
K I E H S I I G V R S R L N S G S E L K

1510 1530 1550
AGAACCGCATGATGATGGGCGCGGACTGGTACGAGACCGAGGACGAGATCTCGAGGCTGA
N A M M M G A D S Y E T E D E I S R L M

1570 1590 1610
TGTC TGAGGCAAGGTTCOCATCGGCGTGGGGAGAACACAAAGATCAGCAACTGCATCA
S E G K V P I G V G E N T K I S N C I I

1630 1650 1670
TOGACATGAACCGGAGGATAGGAAGGGAAGTGGTCATCTCAAACAAGGAGGGGGTGCAAG
D M N A R I G R D V V I S N K E G V Q E

1690 1710 1730
AAGCCGACAGGCCGAGGAAGGGTACTACATCAGGTCCGGATGGTGGTGATCCAGAAGA
A D R P E E G Y Y I R S G I V V I Q K N

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1750 1770 1790
ACGCGACCATCAAGGACGGCACCGTCGTGTAGGGCGTGCCGGGTCCGCGGACGGGGTTC
A T I K D G T V V *
1810 1830 1850
TGGACAACCTGTGCGCTGCGTCGGTGGTCATCATCTTCTCAAACCTCCGGGACTGAAGAA
1870 1890 1910
GTGATCCGGGGACGGGAGACGTTTGAAGCTTGAATGACTGAGACTGAAAGTGAAGGCGCA
1930 1950 1970
GCAGAGGCAGGCAGCATTAGTAGTAAGTAGTAAGTAAGTAGCAGTGAACAAAGTAATAG
1990 2010 2030
TCGTTCTGTTTTTCCCTGTAAATAATAAGAGGCTGTGTGTGTGAGGTAAAAA

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FIG. 15

Nucleotide sequence and derived amino acid sequence of a cDNA encoding the small subunit of ADP-glucose pyrophosphorylase from barley seed endosperm.

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      10              30              50
AAAAGTGAAC TCACACATCACTCAATATCTATATCCTTCCATT TTATATCCCTCGGTGAT
      70              90             110
GGATGTACCTTTGGCATCTAAAGTTCCCTTGCCCTCCCTTCCAAGCATGAACAATGCCAA
D V P L A S K V P L P S P S K H E Q C N
     130             150             170
CGTTTATAGTCATAAGAGCTCATCGAAGCATGCAGATCTCAATCCCCATGCTATTGATAG
V Y S H K S S S K H A D L N P H A I D S
     190             210             230
TGTTCTCGGTATCATTTCTTGGAGGTGGTGCAAGGACTAGATTGTATCCCTGACGAAGAA
V L G I I L G G G A G T R L Y P L T K K
     250             270             290
GGGTGCAAGGCTGCAGTGGCATTGGGTGCCAACTACAGGCTTATTGATATTCTGTGTCAG
R A K P A V P L G A N Y R L I D I P V S
     310             330             350
TAATTGTCTGAACAGCAACATATCAAAGATCTATGTGCTTACACAGTTCAACTCAGCTTC
N C L N S N I S K I Y V L T Q F N S A S
     370             390             410
TCTTAATGTGTCATCTCTCAAGAGCCTATGGGAGCAACATTGGAGGTTACAAGAATGAAGG
L N R H L S R A Y G S N I G G Y K N E G
     430             450             470
ATTGTGTGAAGTCTTCTGCTGCACAGCAGAGGCCAGATAACCCCTGACTGGTTCCAGGGTAC
F V E V L A A Q Q S P D N P D W F Q G T
     490             510             530
TGCAATGCTGTAAAGGCAGTACTTGTGGCTATTTCGAGGACATAATGTTATGGAGTATCT
A D A V R Q Y L W L F E E H N V M E Y L

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550 570 590
AATTCCTTGCTGGAGATCACCTGTACCGAATGGACTATGAAAAGTTTATTTCAGGCACACAG
I L A G D H L Y R M D Y E K F I Q A H R

610 630 650
AGAAACGGATGCTGATATTACTGTGTGCTGCCCTTGCCCATGGATGAGGAACGTGCAACTGC
E T D A D I T V A A L P M D E E R A T A

670 690 710
ATTTCGGCCTTATGAAAATCGATGAAGAAGGGAGGATAATTGAANTTCGACAGAAACCAAA
F G L M K I D E E G R I I E F A E K P K

730 750 770
AGGAGAACAGTTGAAAGCTATGATGGTTGATACGACCATACTTGGCCTTGAAGATGCGAG
G E Q L K A M M V D T T I L G L E D A R

790 810 830
GCCAAAGGAAATGCCCTTATATTGCTAGCATGGGTATCTATGTTATTAGCAAACATGTGAT
A K E M P Y I A S M G I Y V I S K H V M

850 870 890
GCTTCAGCTTCTCCGTGAGCAATTTCTGGAGCTAATGACTTCGGAAGTGAAGTTAT.CC
L Q L L R E Q F P G A N D F G S E V X P

910 930 950
TGGTGCAACTAGCACTGGCATGAGGGTACAAGCATACCTATACGACGGTTACTGGGAAGA
G A T S T G M R V Q A Y L Y D G Y W E D

970 990 1010
TATTGGTACAAATTGAGGCATTCATAATGCAAATTTGGGAATTACCAAAAAACCAATACC
I G T I E A F Y N A N L G I T K K . P I P

1030 1050 1070
TGATTTTCAGTTTCTATGACCGTTCTGCTGCCATTTACACACAACCTCGACACTTGGCTCC
D F S F Y D R S A P I Y T Q P R H L P P

1090 1110 1130
TTCAAAGGTTCTTGATGCTGATGTGACAGACAGTGTAAATTGGTGAAGGATGTGTTATTAA
S K V L D A D V T D S V I G E G C V I K

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1150 1170 1190
AAACTGCAAGATACACCATTTCAGTAGTTGGACTCCGTTCCCTGCATATCTGAAGGTGCAAT
N C K I H H S V V G L R S C I S E G A I

1210 1230 1250
AATAGAGGACACGTTGCTAATGGGTGCGGACTACTATGAGACTGAAGCTGATAAGAACT
I E D T L L M G A D Y Y E T E A D K K L

1270 1290 1310
CCTTGTCTGAAAAAGGTGGCATTCCCATTTGGTATTGGAAAGAAATTCACACATCAAAAGAGC
L A E K G G I P I G I G K N S H I K R A

1330 1350 1370
AATCATTTGACAAGAATGCTCTGTTATTTGGAGATAACGTGATGATAATCAATGTTGACAATGT
I I D K N A R I G D N V M I I N V D N V

1390 1410 1430
TCAAGAAGCGGCGAGGGAGACAGATGGATACTTCATCAAAGTGGCATCGTAACIGTGAT
Q E A A R E T D G Y F I K S G I V T V I

1450 1470 1490
CAAGGATGCTTTACTCCCTAGTGGACAGTCATATGAAGCAGATGTGAAATGTATGCCAA
K D A L L P S G T V I *

1510 1530 1550
AAGACAGGGCTACTTGGTTCAGTCTGGAATCAACCAACAAGGCCGCGAAGGAGATCATAA

1570 1590 1610
AATAAAAA.GGAGTGCCATGCGAGTCACTTCTACACCCCTTTCCCCCTTGATGTATTAG

1630 1650 1670
GAACTGTGATGTACAAGCAACTGTGATGCCTTACGCGAGTGGCCCTGGATTTCAGCTTT

1690 1710 1730
CTCTTTGCTTTGTAAGTGGTTTCCAGCAGACCATGCTATTGTTGTATGGTTCTGTGCAAAA

1750 1770 1790
CCTTGGCATGCTTTATATATGCTTTATATATAAACAAGATGAATCCCCGCGCGTTGCTGC

1810
GGCACAIAAAAAAAAAAAAAAAAAA

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FIG. 16

Nucleotide sequence and derived amino acid sequence of a cDNA
encoding a potato starch branching enzyme.

60
CCCGTCTGTAAGCATCATTAGTGTGTTGCCAGCTGAATGGGATGATTCAGATGCAAA
120
CGTCTGGGGTGAGAACATACAAGAAGGCAGCAGCTGAAGCAAAGTACCATAATTTAATCA
180
ATGGAAATTAATTTCAAAGTTTTATCAAAACCCATTGAGGATCTTTTCCATCTTTCTCA
M E I N F K V L S K P I R G S F P S F S
240
CCTAAAGTTTCTTCAGGGCTTCTAGAAATAAGATATGTTTTCTTCTCAACATAGTACT
P K V S S G A S R N K I C F P S Q H S T
300
GGACTGAAGTTTGGATCTCAGGAACGGTCTTGGGATATTTCTTCCACCCCAAATCAAGA
G L K F G S Q E R S W D I S S T P K S R
360
GTTAGAAAAGATGAAAGGATGAAGCACAGTTCAGCTATTTCCGCTGTTTTGACCGATGAC
V R K D E R M K H S S A I S A V L T D D
420
AATTCGACAATGGCACCCCTAGAGGAAGATGTCAAGACTGAAAATATTGGCCTCCTAAAT
N S T M A P L E E D V K T E N I G L L N
480
TTGGATCCAACCTTTGGAACCTTATCTAGATCACTTCAGACACAGAATGAAGAGATATGTG
L D P T L E P Y L D H F R H R M K R Y V

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FIG. 17

Nucleotide sequence of a tuber specific class I patatin promoter.

60
TTGTTAGTTAATGCGTATTAGTTTTAGCGACGAAGCACTAAATCGTCTTTGTATACTTTC
120
AGTCACACATGTTTAGTGAAGACTGATTGACGAAATTTTTTTCGTCTCACAAAATTTTTA
180
GTGACGAAACATGATTTATAGATGACGAAATTTTGTCCCTCATAATCTAATTTGTGT
240
AGTGATCATTAATCCTTTGTTTGTTTTATTTGTCATGTTAGTTCATTAAAAAAAATCT
300
CTCTTCTTATCAATTCGACGTGTTAATATCATAAGATTAAAAAATATTTAATATATC
360
TTTAATTTAAAGCCACAAAATTTAAATTTCTTCGTTAACATAATTTGTCAAATCAGGCTC
420
AAAGATCGTTTTTCATATCGGAATCAGGATTTTATTTATTCCTTTTAAAAATAAAGAGGTG
480
GTGAGCTAAACAATTTCAAATCTCATCACACATATGGGGTCAGCCACAAAATAAAGAAC
540
GGTTGCAACCGATCTATTATATAATACTAATAAAGAATAGAAAAAGGAAGTGAGTGAGG
600
TGCGAGGGAGAGAATCTGTTTAAATATGCAGAGTCGATCATGIGTCAGTTTTATCGATATC

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660

ACTCTGATTTCAACTGAGTTTAAGCAATTC TGATAAGGCGAGGAAAATCACAGTCCTGAA

720

ATCTAGAAAAATCTCATA CAGTGAGATAAATCTCAACAAAAACGTTGAGTCCATAGAGGG

780

GGTGTATGTGACACCCAACTCAGCAAAAGAAAACCTCCCCCTCAAGAAGGACATTTGCCG

840

TGCTAAACAATTTCAAGTCTCATCACACATATATATTATATAATACTAATAAAGAATAGA

900

AAAAGGAAAGGTAAACATCACTAATGACAGTTGCCGTGCAAAGTGAGTGAGATAATAAAC

960

ATCAGTAATAGACATCACTAACTTTTATTGGTTATGTCCTTCTCAAAATAAAATTTCTCA

1020

ACTTGTTTAAGTGCCATATATATACCATGCTTGTATATGCTCAAAGCACCAACAAAATTT

1047

AAAAACACTTTGAACATTTGCCCCGGG